

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:48:29 ; Search time 12.59 Seconds  
(without alignments)  
321.731 Million cell updates/sec

Title: US-09-828-000-3  
Perfect score: 180  
Sequence: 1 EPAVYFKQFLDGDGWTSRW.....PDNTYEVKIDNSQVSGSLE 180

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 18

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result<br>No. | Score | Query<br>Match | Length | DB | ID | Description |
|---------------|-------|----------------|--------|----|----|-------------|
| -----         |       |                |        |    |    |             |

No matches found

Search completed: January 14, 2002, 08:50:22  
Job time: 113 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:49:15 ; Search time 14.43 Seconds  
(without alignments)  
950.202 Million cell updates/sec

Title: US-09-828-000-3  
Perfect score: 180  
Sequence: 1 EPAVYFKEQFLDGDGWTSRW.....PDNTYEVKIDNSQVESGSL 180

Scoring table:  
OLIGO 60.0 , Gapext 60.0  
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 18

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_58:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 180   | 100.0       | 417    | 1 A37047 | calreticulin precu |
| 2          | 77    | 42.8        | 416    | 1 S05763 | calreticulin precu |
| 3          | 77    | 42.8        | 416    | 2 JH0819 | calreticulin precu |
| 4          | 77    | 42.8        | 418    | 1 A34154 | calreticulin precu |
| 5          | 62    | 34.4        | 400    | 2 S43376 | calreticulin, brai |
| 6          | 62    | 34.4        | 421    | 2 S36799 | calreticulin precu |
| 7          | 27    | 15.0        | 405    | 1 JH0795 | calreticulin precu |
| 8          | 22    | 12.2        | 384    | 2 S29130 | calreticulin (clon |
| 9          | 22    | 12.2        | 411    | 2 S29129 | calreticulin precu |
| 10         | 20    | 11.1        | 419    | 2 S71343 | calreticulin precu |
| 11         | 19    | 10.6        | 336    | 2 A32507 | 41K larval antigen |
| 12         | 19    | 10.6        | 406    | 2 A56637 | calreticulin homol |

#### ALIGNMENTS

RESULT 1  
A37047  
calreticulin precursor - human  
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prote  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075  
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.  
J. Biol. Chem. 267, 2557-2562, 1992  
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with the  
A:Reference number: A42330; MUID:92129342  
A:Accession: A42330

A:Molecule type: DNA  
A:Residues: 1-417 <MC2>  
A:Note: Sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)  
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin  
J. Clin. Invest. 85, 1379-1391, 1990  
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/  
A:Reference number: A37047; MUID:90237213  
A:Accession: A37047  
A:Molecule type: mRNA  
A:Residues: 1-417 <MC2>  
A:Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487  
A:Note: the authors translated the codon GTA for residue 349 as Tyr  
R:Rokach, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.  
J. Immunol. 147, 3031-3039, 1991  
A:Title: Characterization of the autoantigen calreticulin.  
A:Reference number: A46452; MUID:92013129  
A:Accession: A46452  
A:Molecule type: mRNA  
A:Residues: 1-417 <ROK>  
A:Cross-references: GB:M84739; NID:gl79881; PIDN:AAA51916.1; PID:gl79882  
A:Note: Sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)  
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.  
J. Clin. Invest. 82, 96-101, 1988  
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence  
A:Reference number: A28812; MUID:88273610  
A:Accession: A28812  
A:Molecule type: protein  
A:Residues: 18-41 <LIE>  
A:Note: 18-Ala was also found  
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschoep, J.  
J. Exp. Med. 177, 1-7, 1993  
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra  
A:Reference number: PH1525; MUID:93115648  
A:Accession: PH1525  
A:Molecule type: protein  
A:Residues: 18-27 <DUP>  
A:Experimental source: LAK cell  
R:Roiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.  
Biochemistry 30, 9859-9866, 1991  
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c  
A:Reference number: A40346; MUID:9202034  
A:Accession: A40346  
A:Molecule type: protein  
A:Residues: 18-34,'R' <ROJ>  
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.  
Biochem. J. 270, 545-548, 1990  
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that corpu  
A:Reference number: S11475; MUID:90380058  
A:Accession: S11475  
A:Molecule type: protein  
A:Residues: 18-32 <KRA>  
R:Lamerdin, J.; McGready, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.  
Submitted to the EMBL data Library, November 1996  
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb re  
A:Reference number: Z22906  
A:Accession: T45075  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-417 <LAM>  
A:Cross-references: EMBL:AD000092; PIDN:AAB51176.1  
A:Experimental source: cell line 5HL2-B; fibroblast  
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome a  
C:Genetics:  
A:Gene: GDB:CALR  
A:Cross-references: GDB:125179; OMIM:109091  
A:Map position: 19p13.3-19p13.2  
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 273/3; 320/3; 351/3  
A:Note: CRTG  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; integrin binding  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-417/Product: calreticulin #status predicted <MAT>  
F;414-417/Region: endoplasmic reticulum retention signal

RESULT 3

JH0819

calreticulin precursor - rat

N;Alternate names: calcium-binding protein 3

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1993 #sequence,revision 20-Aug-1994 #text change 20-Jun-2000

C;Accession: JH0819, A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045

R;Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, T.

Exp. Cell Res. 205, 101-110, 1993

A;Title: An endoplasmic reticulum protein, calreticulin, is transported into the acro-

A;Reference number: A49176; MUID:93202172

A;Accession: JH0819

A;Molecule type: mRNA

A;Residues: 1-416 <NAK>

A;Cross-references: GB:D78308; NID:g1089798; PIDN:BAAL1345.1; PID:g1845572

A;Accession: A49176

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-416 <NA2>

A;Cross-references: GB:D78308; NID:g1089798; PIDN:BAAL1345.1; PID:g1845572

A;Experimental source: Sprague-Dawley, spermatogenic cells

A;Note: Sequence extracted from NCBI backbone (NCBI:127639, NCBI:127643)

R;Murthy, K.K.; Banville, D.; Srikanth, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel

Nucleic Acids Res. 18, 4933, 1990

A;Title: Structural homology between the rat calreticulin gene product and the Oncho-

A;Reference number: S11205; MUID:90370456

A;Accession: S11205

A;Molecule type: mRNA

A;Residues: 1-416 <MR>

A;Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855

R;Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.

Biochem. Biophys. Res. Commun. 186, 668-673, 1992

A;Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.

A;Reference number: PC1109; MUID:92360010

A;Accession: PC1109

A;Molecule type: protein

A;Residues: 18-32 <NAK2>

A;Experimental source: testis, strain Sprague-Dawley

R;Soennichsen, B.; Fueillekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mies

submitted to the EMBL Data Library, May 1994

A;Description: Retention and retrieval: both mechanisms cooperate to maintain calreti-

A;Reference number: S45036

A;Accession: S45036

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-416 <SOE>

A;Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841

R;Ione, Y.C.; Bailly, A.; Lutruffe, N.

submitted to the EMBL Data Library, December 1988

A;Reference number: S04867

A;Accession: S04867

A;Molecule type: mRNA

A;Residues: R' 270-358, 'RAG' <LON>

A;Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260

A;Note: The authors designated the protein as D-beta-hydroxybutyrate dehydrogenase

R;Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kanetaki, T.

Biochim. Biophys. Acta 1150, 339-344, 1993

A;Title: Identification of protein disulfide isomerase and calreticulin as autoimmune

A;Reference number: S39371; MUID:94072621

A;Accession: S39372

A;Molecule type: protein

A;Residues: 18-23, 'X', 25-32 <YOK>

R;Van, P.N.; Peter, F.; Soeling, H.D.

J. Biol. Chem. 264, 17494-17501, 1989

A;Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes

active calcium sequestering rat liver vesicles.

A;Reference number: A34473; MUID:90008920

A;Accession: A34473

A;Status: preliminary

A;Molecule type: protein

A;Residues: 18-36 <VAN>

R;Reves, S.; de Mattei, M.; Lanfretti, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M

Biochem. J. 271, 473-480, 1990

A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
A;Reference number: S13045; MUID:91054414  
A;Accession: S13045  
A;Molecule type: protein  
A;Residues: 18-29 <PRE>  
C;Superfamily: calreticulin  
C;Keywords: calcium binding; glycoprotein  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-416/Product: calreticulin #status experimental <MAT>  
F;204-212/Region: nuclear location signal  
F;413-416/Region: endoplasmic reticulum retention signal  
F;344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.8%; Score 77; DB 2; Length 416;  
Best Local Similarity 100.0%; Pred. No. 5.2e-74;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDSEYNMFPGDTCGPGTKKVHVFYKGNVINKDIRCKDDFFTHLYTLIVRPN 163  
|||||  
Db 121 DMHGDSEYNMFPGDTCGPGTKKVHVFYKGNVINKDIRCKDDFFTHLYTLIVRPN 180  
|||||

QY 164 TYEVKIDNSQVESGSL 180  
|||||  
Db 181 TYEVKIDNSQVESGSL 197  
|||||

RESULT 4  
A34154  
calreticulin precursor, skeletal muscle - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
A;Accession: A34154; S13047  
R;Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.  
J. Biol. Chem. 264, 21522-21528, 1989  
A;Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) c  
A;Reference number: A34154; MUID:90094320  
A;Accession: A34154  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-418 <FLI>  
A;Cross-references: GB:J05138; NID:gl64858; PIDN:AAA31188.1; PID:gl64859  
R;Treves, S.; de Mattel, M.; Lanfretti, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld  
Biochem. J. 271, 473-480, 1990  
A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
A;Reference number: S13045; MUID:91054414  
A;Accession: S13047  
A;Molecule type: protein  
A;Residues: 19-32 <PRE>  
C;Superfamily: calreticulin  
C;Keywords: skeletal muscle  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;415-418/Region: endoplasmic reticulum retention signal

Query Match 42.8%; Score 77; DB 1; Length 418;  
Best Local Similarity 100.0%; Pred. No. 5.2e-74;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDSEYNMFPGDTCGPGTKKVHVFYKGNVINKDIRCKDDFFTHLYTLIVRPN 163  
|||||  
Db 121 DMHGDSEYNMFPGDTCGPGTKKVHVFYKGNVINKDIRCKDDFFTHLYTLIVRPN 180  
|||||

QY 164 TYEVKIDNSQVESGSL 180  
|||||  
Db 181 TYEVKIDNSQVESGSL 197  
|||||

RESULT 5  
S43376  
calreticulin, brain isoform 1 - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Oct-1994 #sequence\_revision 23-Mar-1995 #text\_change 07-May-1999

C;Accession: S43376; S36801  
R;Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.  
Biochem. J. 298, 435-442, 1994  
A;Title: Covalent structure of bovine brain calreticulin.  
A;Reference number: S43376; MUID:94183174  
A;Accession: S43376  
A;Molecule type: protein  
A;Residues: 1-400 <MAT>  
A;Experimental source: brain  
R;Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli  
A;Reference number: S36799; MUID:93385184  
A;Accession: S36801  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 45-63, E', 65-83 <LIU>  
A;Experimental source: brain, clone 8.1  
C;Superfamily: calreticulin  
C;Keywords: calcium binding; glycoprotein  
F;397-400/Region: endoplasmic reticulum retention signal  
F;120-146/Disulfide bonds: #status experimental  
F;162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 34.4%; Score 62; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 5e-58;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LDQTDHMGDSEYNMFPGDTCGPGTKKVHVFYKGNVINKDIRCKDDFFTHLYTLIV 159  
|||||  
Db 100 LDQTDHMGDSEYNMFPGDTCGPGTKKVHVFYKGNVINKDIRCKDDFFTHLYTLIV 159  
|||||

QY 160 RP 161  
||  
Db 160 RP 161  
||

RESULT 6  
S36799  
calreticulin precursor, brain isoform 2 - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 10-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 13-Aug-1999  
A;Accession: S36799; S36800  
R;Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli  
A;Reference number: S36799; MUID:93385184  
A;Accession: S36799  
A;Molecule type: mRNA  
A;Residues: 1-421 <LIU>  
A;Cross-references: GB:L13462; NID:g348693; PIDN:AAC37307.1; PID:g348694  
A;Experimental source: brain, clone 9.4  
A;Accession: S36800  
A;Molecule type: protein  
A;Residues: 35-45 <LI2>  
C;Superfamily: calreticulin  
C;Keywords: calcium binding; glycoprotein  
F;1-34/Domain: signal sequence #status predicted <SIG>  
F;35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>  
F;418-421/Region: endoplasmic reticulum retention signal  
F;141-167/Disulfide bonds: #status predicted  
F;183/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.4%; Score 62; DB 2; Length 421;  
Best Local Similarity 100.0%; Pred. No. 5.2e-58;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LDQTDHMGDSEYNMFPGDTCGPGTKKVHVFYKGNVINKDIRCKDDFFTHLYTLIV 159  
|||||  
Db 121 LDQTDHMGDSEYNMFPGDTCGPGTKKVHVFYKGNVINKDIRCKDDFFTHLYTLIV 180  
|||||

QY 160 RP 161  
||  
Db 181 RP 182

RESULT 7  
JH0795  
calreticulin precursor - California sea hare  
N:Alternate names: protein 407  
C:Species: Aplysia californica (California sea hare)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JH0795; B31409; F60977  
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.  
Neuron 9, 1013-1024, 1992  
A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin  
in aplysia.  
A:Reference number: JH0795; MUID:93098937  
A:Accession: JH0795  
A:Molecule type: mRNA  
A:Residues: 1-405 <KEN>  
A:Cross-references: GB:S51239; NID:g262053; PIDN:AAB24569.1; PID:g262054  
A:Experimental source: abdominal ganglion and antral nervous system  
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988  
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and  
tion in Aplysia.  
A:Reference number: A94207; MUID:88320566  
A:Accession: B31409  
A:Molecule type: protein  
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>  
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.  
Electrophoresis 10, 152-157, 1989  
A:Title: Development of a database of amino acid sequences for proteins identified and  
A:Reference number: A60977; MUID:89276264  
A:Accession: F60977  
A:Molecule type: protein  
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-405/Product: calreticulin #status experimental <MAT>  
F:402-405/Region: endoplasmic reticulum retention signal

Query Match 15.0%; Score 27; DB 1; Length 405;  
Best Local Similarity 100.0%; Pred. No. 1.1e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 YNIMGPDICGPGTKVHVFNKGN 137  
|||  
Db 124 YNIMGPDICGPGTKVHVFNKGN 150  
|||

RESULT 8  
S29130  
calreticulin (clone 8) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29130; T01068  
R:Truves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992  
A:Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997  
A:Accession: S29130  
A:Molecule type: mRNA  
A:Residues: 1-384 <TRV>  
A:Cross-references: EMBL:X67598  
A:Accession: T01068  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-339, 'XTGR' <TRV>  
A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611  
A:Experimental source: CNS  
C:Superfamily: calreticulin

C:Keywords: glycoprotein  
F:381-384/Region: endoplasmic reticulum retention signal  
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.2%; Score 22; DB 2; Length 384;  
Best Local Similarity 100.0%; Pred. No. 2.2e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 FTHLYTLIVRPDNTYEVKIDNS 172  
|||  
Db 140 FTHLYTLIVRPDNTYEVKIDNS 161  
|||

RESULT 9  
S29129  
calreticulin precursor (clone 3) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: S29129  
R:Truves, S.; Zorzato, F.; Pozzan, T.  
Biochem. J. 287, 579-581, 1992  
A:Title: Identification of calreticulin isoforms in the central nervous system.  
A:Reference number: S29129; MUID:93074997  
A:Accession: S29129  
A:Molecule type: mRNA  
A:Residues: 1-411 <TRE>  
A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609  
C:Superfamily: calreticulin  
C:Keywords: glycoprotein  
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>  
F:13-411/Product: calreticulin #status predicted <MAT>  
F:408-411/Region: endoplasmic reticulum retention signal  
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.2%; Score 22; DB 2; Length 411;  
Best Local Similarity 100.0%; Pred. No. 2.4e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 FTHLYTLIVRPDNTYEVKIDNS 172  
|||  
Db 163 FTHLYTLIVRPDNTYEVKIDNS 184  
|||

RESULT 10  
S71343  
calreticulin precursor - Korean frog  
C:Species: Rana rugosa (Korean frog)  
C:Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 20-Jun-2000  
C:Accession: S71343  
R:Yamamoto, S.; Nakamura, M.  
FEBS Lett. 387, 27-32, 1996  
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Ran  
A:Reference number: S71342; MUID:96234004  
A:Accession: S71343  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-419 <YAM>  
A:Cross-references: EMBL:D78589; NID:gl514956; PIDN:BAAL1425.1; PID:gl514957  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; endoplasmic reticulum  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-419/Product: calreticulin #status predicted <MAT>  
F:205-213/Region: nuclear location signal  
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 11.1%; Score 20; DB 2; Length 419;  
Best Local Similarity 100.0%; Pred. No. 3.3e-13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 HLYTLIVRPDNTYEVKIDNS 172

Search completed: January 14, 2002, 08:51:14  
Job time: 119 sec

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Db 171 HLYTLIVRPDNTYEVKIDNS 190
|||||
RESULT 11
A32507
41K larval antigen - nematode (Onchocerca volvulus) (fragment)
C:Species: Onchocerca volvulus
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
C:Accession: A32507; A28813
R:Unnasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Erttmann, K.D.; Greene, B.M.
J. Clin. Invest. 82, 262-269, 1988
A:Title: Isolation and characterization of expression cDNA clones encoding antigens of O.
A:Reference number: A92769; MUID:88273584
A:Accession: A32507
A:Molecule type: mRNA
A:Residues: 1-336 <UNN>
C:Superfamily: calreticulin

Query Match 10.6%; Score 19; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKKVVHVF 131
|||||
Db 76 IMFGPDICGPGTKKVVHVF 94

RESULT 12
A56637
calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C:Species: Drosophila melanogaster
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C:Accession: A56637; A37158
R:Smith, M.J.
DNA Seq. 3, 247-250, 1992
A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin h
A:Reference number: A56637; MUID:93208374
A:Accession: A56637
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <SMI>
A:Cross-references: GB:X64461; NID:97685; PIDN:CAA45791.1; PID:97686
A>Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBIIP:128275)
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.
J. Clin. Invest. 86, 332-335, 1990
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom
A:Reference number: A37158; MUID:90307981
A:Accession: A37158
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 91-105, 'A', 107, 109-124; 182-183, 'L', 185-220 <MCC>
C:Genetics:
A:Gene: FlyBase:Crc
A:Cross-references: FlyBase:FBgn0005585
A:Introns: 65/1; 222/3
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-17/Domain: signal sequence #status predicted <SIG>
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 10.6%; Score 19; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKKVVHVF 131
|||||
Db 130 IMFGPDICGPGTKKVVHVF 148
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:49:34 ; Search time 11.77 Seconds  
(without alignments)  
560.720 Million cell updates/sec

Title: US-09-828-000-3  
Perfect score: 180  
Sequence: 1 EPAYVKEQFLDGDGWTSRM.....PONTVEYKIDNSQVSGSLE 180

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 18

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 180   | 100.0       | 417    | 1     | CRTC_HUMAN  |
| 2          | 77    | 42.8        | 416    | 1     | CRTC_MOUSE  |
| 3          | 77    | 42.8        | 416    | 1     | CRTC_RAT    |
| 4          | 77    | 42.8        | 418    | 1     | CRTC_RABBIT |
| 5          | 62    | 34.4        | 400    | 1     | CRT1_BOVIN  |
| 6          | 62    | 34.4        | 421    | 1     | CRT2_BOVIN  |
| 7          | 25    | 13.9        | 105    | 1     | CRTC_PIG    |
| 8          | 19    | 10.6        | 388    | 1     | RALI_ONCVO  |
| 9          | 19    | 10.6        | 406    | 1     | CRTC_DROME  |

#### ALIGNMENTS

RESULT 1  
ID CRTC\_HUMAN STANDARD; PRT; 417 AA.  
AC P27797;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA  
DE RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).  
GN CALR OR CRTC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92013129; PubMed=1919005;  
RA Rokeach L.A., Hazelby J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,  
RA Greene B.M., Hoch S.O.;

RT "Characterization of the autoantigen calreticulin.";  
RL J. Immunol. 147:3031-3039(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90237213; PubMed=2332496;  
RA McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,  
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,  
RA Capra J.D.;  
RT "Molecular cloning, expression, and chromosome 19 localization of a  
RT human Ro/SS-A autoantigen.";  
RL J. Clin. Invest. 85:1379-1391(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92129342; PubMed=1733953;  
RA McCaulliffe D.P., Yang Y.S., Willson J., Sontheimer R.D., Capra J.D.;  
RT "The 5'-flanking region of the human calreticulin gene shares  
RT homology with the human GRP78, GRP94, and protein disulfide isomerase  
RT promoters.";  
RL J. Biol. Chem. 267:2557-2562(1992).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 18-36.  
RX MEDLINE=92002034; PubMed=1911778;  
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;  
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A  
RT antigen (calreticulin) with a highly conserved amino acid sequence in  
RT the cytoplasmic domain of integrin alpha subunits.";  
RL Biochemistry 30:9859-9866(1991).  
RN [6]  
RP SEQUENCE OF 18-32.  
RX MEDLINE=90380058; PubMed=2400400;  
RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;  
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein  
RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60  
RT cells.";  
RL Biochem. J. 270:545-548(1990).  
RN [7]  
RP SEQUENCE OF 18-28.  
RC TISSUE=Liver;  
RX MEDLINE=93162045; PubMed=1286669;  
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,  
RA Appel R.D., Hughes G.J.;  
RT "Human liver protein map: a reference database established by  
RT microsequencing and gel comparison.";  
RL Electrophoresis 13:992-1001(1992).  
RN [8]  
RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.  
RC TISSUE=Keratinocytes;  
RX MEDLINE=93162043; PubMed=1286667;  
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
RA Vandekerckhove J.;  
RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
RT protein database of normal human epidermal keratinocytes.";  
RL Electrophoresis 13:960-969(1992).  
RN [9]  
RP SEQUENCE OF 18-26.  
RC TISSUE=Colon carcinoma;  
RX MEDLINE=97295306; PubMed=9150948;  
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
RT "A two-dimensional gel database of human colon carcinoma proteins.";  
RL Electrophoresis 18:605-613(1997).  
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC LOW AFFINITY CALCIUM-BINDING SITES.  
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration



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FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 42.8%; Score 77; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 9e-72;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDSEYNIMFGDPCGCTKKVHVFNKGNVLNKDIRCKDDFTHLYTLIVRPDN 163
DB 121 DMHGDSEYNIMFGDPCGCTKKVHVFNKGNVLNKDIRCKDDFTHLYTLIVRPDN 180
QY 164 TYEVKIDNSQVESGSLE 180
DB 181 TYEVKIDNSQVESGSLE 197

RESULT 3
ID CRTCL_RAT STANDARD; PRT; 416 AA.
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)
DE (CALCIUM-BINDING PROTEIN 3) (CABP3).
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain cortex;
RX MEDLINE=90370496; PubMed=2395661;
RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A.,
RA Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and
RL the Onchocerca volvulus antigen Rel-1."
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
RA Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into
RL the acrosome of rat sperm."
RL Exp. Cell Res. 205:101-110(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=95181573; PubMed=7876339;
RA Soennichsen B., Fueflekrug J., van Nguyen P., Diekmann W.,
RA Robinson D.G., Mieskes G.;
RT "Retention and retrieval: both mechanisms cooperate to maintain
RL calreticulin in the endoplasmic reticulum."
RL J. Cell Sci. 107:2705-2717(1994).
RN [4]
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Lone Y.C., Bailly A., Latruffe N.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 18-29.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
RL Ca2(+)-storage compartments (calciosomes) of liver and brain."
RL Biochem. J. 271:473-480(1990).
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RN RP SEQUENCE OF 18-32.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
RX MEDLINE=92360010; PubMed=1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RT "Calreticulin is present in the acrosome of spermatids of rat
RL testis."
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
RP SEQUENCE OF 18-32.
RC STRAIN=LEC; TISSUE=Liver;
RX MEDLINE=94072621; PubMed=8251535;
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
RA Kamataki T.;
RT "Identification of protein disulfide isomerase and calreticulin as
RL autoimmune antigens in LEC strain of rats."
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
CC HYDROXYBUTYRATE DEHYDROGENASE.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D78308; BA011345.1; -
DR EMBL; X53363; CAA37446.1; -
DR EMBL; X13702; CAA31987.1; ALT_SEQ.
DR EMBL; X79327; CAA35890.1; -
DR PIR; S04867; S04867.
DR PIR; S11205; S11205.
DR PIR; S13045; S13045.
DR PIR; A49176; A49176.
DR PIR; S45036; S45036.
DR PIR; JH0819; JH0819.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;
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Query Match 42.8%; Score 77; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 9e-72;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGSEYNIMFGPDICGPGTKKVVIFNYKGNVLINKDIRCKDDETHLYTLIVRPD 163
DB 121 DMHGSEYNIMFGPDICGPGTKKVVIFNYKGNVLINKDIRCKDDETHLYTLIVRPD 180

QY 164 TYEVKIDNSQVSGSLE 180
DB 181 TYEVKIDNSQVSGSLE 197

RESULT 4
CRTC_RABIT
ID CRTC_RABIT STANDARD; PRT; 418 AA.
AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
GN CALR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID-9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Slow-twitch skeletal muscle;
RX MEDLINE-90094320; PubMed-2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
(calreticulin) of skeletal muscle sarcoplasmic reticulum.";
RL J. Biol. Chem. 264:21522-21528(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Fast-twitch skeletal muscle;
RX MEDLINE-91128795; PubMed-2059224;
RA Fliegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
RN [3]
RP SEQUENCE OF 18-36.
RX MEDLINE-91054414; PubMed-2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [4]
RP SEQUENCE OF 18-46.
RX MEDLINE-91201375; PubMed-2016321;
RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
RN [5]
RP PARTIAL SEQUENCE.
RX TISSUE-Lung;
RX MEDLINE-92002038; PubMed-1911780;
RA Guan S., Falick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
monooxygenase and calreticulin.";
CC Biochemistry 30:9892-9900(1991).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
-----
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or send an email to license@isb-sib.ch).
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CC EMBL; J05138; AAA31188.1; -.
CC PIR; A34154; A34154.
CC PIR; C33208; C33208.
CC PIR; D33208; D33208.
CC PIR; E33208; E33208.
CC PIR; F33208; F33208.
CC PIR; S13046; S13046.
CC PIR; S13047; S13047.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR000886; ER_target.
CC Pfam; PF00262; calreticulin_1.
CC PRINTS; PR00626; CALRETICULIN.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW SIGNAL
FT CHAIN 1 17
FT DOMAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 42.8%; Score 77; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 9e-72;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGSEYNIMFGPDICGPGTKKVVIFNYKGNVLINKDIRCKDDETHLYTLIVRPD 163
DB 121 DMHGSEYNIMFGPDICGPGTKKVVIFNYKGNVLINKDIRCKDDETHLYTLIVRPD 180

QY 164 TYEVKIDNSQVSGSLE 180
DB 181 TYEVKIDNSQVSGSLE 197

RESULT 5
CRTL_BOVIN
ID CRTL_BOVIN STANDARD; PRT; 400 AA.
AC P52193;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos.
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OX NCB1_TaxID=9913;
RN [1]
RP SEQUENCE.
RC MEDLINE=94183174; PubMed=8135753;
RX Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin.";
RL Biochem. J. 298:435-442(1994).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PROSITE: PS001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT DOMAIN 1 180 N-DOMAIN.
FT DOMAIN 181 291 P-DOMAIN.
FT DOMAIN 292 400 C-DOMAIN.
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.
FT REPEAT 193 204 1-2.
FT REPEAT 210 221 1-3.
FT REPEAT 227 238 1-4.
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
FT DISULFID 120 146 N-LINKED (GLCNAC. . .).
FT CARBOHYD 162 162 PREVENT SECRETION FROM ER (POTENTIAL).
FT SITE 397 400
SQ SEQUENCE 400 AA; 46381 NW; 7D4B68DFC689EEF1 CRC64;

Query Match 34.4%; Score 62; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LDQTMHGDSEYNIMFGPDICGPGTKKVVIFNYKGNVLINKDIRCKDDEFTHLYTLIV 159
Db |||||
QY 160 RP 161
Db 160 RP 161

RESULT 6
CRT2_BOVIN STANDARD; PRT; 421 AA.
AC P42918.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCB1_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
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RT "Comparison of cDNAs from bovine brain coding for two isoforms of
calreticulin.";
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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or send an email to license@isb-sib.ch).
DR EMBL: L13462; AAC37307.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PROSITE: PS001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34 POTENTIAL.
FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
FT DOMAIN 35 201 N-DOMAIN.
FT DOMAIN 202 312 P-DOMAIN.
FT DOMAIN 313 421 C-DOMAIN.
FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
FT REPEAT 195 206 1-1.
FT REPEAT 214 225 1-2.
FT REPEAT 231 242 1-3.
FT REPEAT 248 259 1-4.
FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
FT REPEAT 263 273 2-1.
FT REPEAT 277 287 2-2.
FT REPEAT 291 301 2-3.
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT DISULFID 141 167 BY SIMILARITY.
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 34.4%; Score 62; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.7e-56;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LDQTMHGDSEYNIMFGPDICGPGTKKVVIFNYKGNVLINKDIRCKDDEFTHLYTLIV 159
Db |||||
QY 160 RP 161
Db 160 RP 161

RESULT 7
CRT2_PIG STANDARD; PRT; 105 AA.
AC P28491.
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
DE (FRAGMENT).
GN CALR.
OS Sus scrofa (Pig).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129;
RA Winterroo A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RL library: analysis of 839 clones.";
RM Mamm. Genome 7:509-517(1996).
RN [2]
RP SEQUENCE OF 18-32.
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
RL reticulum.";
RJ J. Biol. Chem. 266:7185-7165(1991).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
-----
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-----
DR EMBL; F14591; CAA23142.1; -.
DR PIR; B33208; B33208.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; PARTIAL.
DR Endoplasmic reticulum; Calcium-binding; Signal.
FT SIGNAL 1 17
FT CHAIN 18 >105 CALRETICULIN.
FT DOMAIN 18 >105 N-DOMAIN.
FT NON_TER 105 105
FT SEQUENCE 105 AA; 11958 MW; D203B53FE36BDE1E CRC64;

Query Match 13.9%; Score 25; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 PEPFSNKGQTLVQFTVKHEQNIDC 88
Db 81 PEPFSNKGQTLVQFTVKHEQNIDC 105
|||||
RESULT 8
RALL_ONCVO
ID RALL_ONCVO STANDARD; PRT; 388 AA.
AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).
GN RALL.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
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RN SEQUENCE FROM N.A.
RP MEDLINE=94341871; PubMed=7520419;
RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the
RT calreticulin family of proteins, recognized by sera from patients
RT with onchocerciasis.";
RL Infect. Immun. 62:3696-3704(1994).
RN [2]
RP SEQUENCE OF 53-388 FROM N.A.
RX MEDLINE=88273584; PubMed=2455736;
RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Ertmann K.D., Greene B.M.;
RT "Isolation and characterization of expression cDNA clones encoding
RT antigens of Onchocerca volvulus infective larvae.";
RL J. Clin. Invest. 82:262-269(1988).
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
-----
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-----
DR EMBL; M20565; AAA59056.1; -.
DR PIR; A32507; A32507.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR Calcium-binding; Repeat; Antigen; Signal.
KW SIGNAL 1 17
FT CHAIN 18 388
FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.
FT REPEAT 189 200 1-1.
FT REPEAT 208 219 1-2.
FT REPEAT 225 236 1-3.
FT REPEAT 242 253 1-4.
FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.
FT REPEAT 271 281 2-1.
FT REPEAT 285 295 2-2.
FT REPEAT 353 388 ARG/LYS-RICH (BASIC).
FT DOMAIN 135 161 BY SIMILARITY.
FT DISULFID 135 161
FT SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;

Query Match 10.6%; Score 19; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. No. 5.8e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 IMFGPDICGPGTKKVHVIF 131
Db 128 IMFGPDICGPGTKKVHVIF 146
|||||
RESULT 9
CRTC_DROME
ID CRTC_DROME STANDARD; PRT; 406 AA.
AC P29413; OSVHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
```

Search completed: January 14, 2002, 08:51:32  
Job time: 118 sec

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GenCore.version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: January 14, 2002, 08:50:09 ; Search time 23.48 Seconds  
(without alignments)  
1121.338 Million cell updates/sec  
Title: US-09-828-000-3  
Perfect score: 180  
Sequence: 1 EPAVYFKEQFLDGDGWTGRW.....PNTYEVKIDNSQVESGSLE 180  
Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 473505 seqs, 146272329 residues  
Word size : 18  
Total number of hits satisfying chosen parameters: 11  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 45 summaries  
Database : SPTREMBL17.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID     | Description         |
|------------|-------|-------|--------|----|--------|---------------------|
| 1          | 27    | 15.0  | 214    | 4  | Q9UDG2 | Q9udg2 homo sapien  |
| 2          | 27    | 15.0  | 405    | 5  | Q26268 | Q26268 aplysia cal  |
| 3          | 27    | 15.0  | 421    | 5  | Q9U6S0 | Q9u6s0 strongyloce  |
| 4          | 25    | 13.9  | 318    | 13 | Q9PRX7 | Q9ptx7 lampetra re  |
| 5          | 24    | 13.3  | 410    | 5  | Q16893 | Q16893 amblyomma a  |
| 6          | 22    | 12.2  | 343    | 13 | Q91711 | Q91711 xenopus lae  |
| 7          | 22    | 12.2  | 411    | 13 | Q91710 | Q91710 xenopus lae  |
| 8          | 21    | 11.7  | 387    | 5  | Q97372 | Q97372 dirofilaria  |
| 9          | 20    | 11.1  | 419    | 13 | Q98984 | Q98984 rana rugosa  |
| 10         | 19    | 10.6  | 375    | 5  | Q18478 | Q18478 litomosolide |
| 11         | 19    | 10.6  | 406    | 5  | Q9U916 | Q9u916 drosophila   |

ALIGNMENTS

RESULT 1  
Q9UDG2 PRELIMINARY; PRT; 214 AA.

AC Q9UDG2;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE CALRETICULIN-CALCIUM BINDING PROTEIN (FRAGMENTS).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95143082; PubMed=7841019;  
RA Houen G., Koch C.;  
RT "Human placental calreticulin: purification, characterization and association with other proteins";  
RL Acta Chem. Scand. 48:905-911(1994).  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 3.  
DR ProDom; PD001866; Calreticulin; 1.  
FT NON\_TER 1 1  
FT NON\_CONS 31 32  
FT NON\_CONS 59 60  
FT NON\_CONS 78 79  
FT NON\_CONS 116 117  
FT NON\_TER 214 214  
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 15.0%; Score 27; DB 4; Length 214;  
Best Local Similarity 100.0%; Pred. No. 4e-21;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPAVYFKEQFLDGDGWTGRWIESKHKS 27  
Db 1 EPAVYFKEQFLDGDGWTGRWIESKHKS 27

RESULT 2

ID Q26268 PRELIMINARY; PRT; 405 AA.  
AC Q26268;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE CALRETICULIN.  
OS Aplysia californica (California sea hare).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspiidea;  
OC Aplysiidae; Aplysia.  
OX NCBI\_TaxID=6500;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93098937; PubMed=1463604;  
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;  
RT "Long-term sensitization training in Aplysia leads to an increase in calreticulin, a major presynaptic calcium-binding protein.";  
RL Neuron 9:1013-1024(1992).  
DR EMBL; S51239; AAB24569.1; -;  
DR InterPro; IPR000886; ER\_target.  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; Calreticulin; 1.  
DR PROSITE; PS00804; CALRETICULIN\_1; 1.  
DR PROSITE; PS00805; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE; PS0014; ER\_TARGET; UNKNOWN\_1.  
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 15.0%; Score 27; DB 5; Length 405;  
Best Local Similarity 100.0%; Pred. No. 6.8e-21;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 YNMFPGDICGPGTKKVHVFYKGN 137  
 |||||  
 Db 124 YNMFPGDICGPGTKKVHVFYKGN 150  
 |||||  
 RESULT 3  
 Q9U6S0 PRELIMINARY; PRT; 421 AA.  
 AC Q9U6S0;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE CALRETICULIN PRECURSOR.  
 GN CALRET.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinozoa; Euechinozoa; Echinacea; Echinoida; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxID=7668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Susan J.M., Just M.L., Lonnarz W.J.;  
 RT "Cloning and Characterization of Alpha Integrin and Calreticulin in  
 Embryos of the Sea Urchin.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DE EMBL: AF177915; AAD55725.1; -;  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR ProDom; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 421 CALRETICULIN.  
 FT TAG 421  
 SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;  
 Query Match 15.0%; Score 27; DB 5; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 7e-21;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 111 YNMFPGDICGPGTKKVHVFYKGN 137  
 |||||  
 Db 127 YNMFPGDICGPGTKKVHVFYKGN 153  
 |||||  
 RESULT 4  
 Q9PTX7 PRELIMINARY; PRT; 318 AA.  
 AC Q9PTX7;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE CALRETICULIN (FRAGMENT).  
 OS Lampetra releaseeri.  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Lampetra.  
 OX NCBI\_TaxID=7753;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-20063780; PubMed:10594174;  
 KX Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;  
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded  
 genes.";  
 RL J. Mol. Evol. 49:729-735(1999).  
 DR EMBL: AB025328; BAA88481.1; -;  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.

DR ProDom; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 318 AA; 36997 MW; C88102EALCAC1506 CRC64;  
 Query Match 13.9%; Score 25; DB 13; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-19;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 113 IMFGPDICGPGTKKVHVFYKGN 137  
 |||||  
 Db 29 IMFGPDICGPGTKKVHVFYKGN 53  
 |||||  
 RESULT 5  
 Q16893 PRELIMINARY; PRT; 410 AA.  
 AC Q16893;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-JAN-1999 (TRENBLrel. 09, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE CALRETICULIN.  
 GN CRT-1.  
 OS Amblyomma americanum.  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.  
 OX NCBI\_TaxID=6943;  
 RN [1]  
 RP SEQUENCE OF 49-410 FROM N.A.  
 RC TISSUE-SALIVARY GLANDS;  
 RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,  
 RT Needham G.R.;  
 RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)  
 saliva.";  
 RL J. Insect Physiol. 41:369-375(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SALIVARY GLANDS;  
 RA Jaworski D.C.;  
 RN Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SALIVARY GLANDS;  
 RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U07708; AAC79094.1; -;  
 DR InterPro: IPR000886; ER\_target.  
 DR InterPro: IPR001580; Calreticulin.  
 DR Pfam: PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR ProDom; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
 SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;  
 Query Match 13.3%; Score 24; DB 5; Length 410;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 73 TLVVQFTVKHEQNIDCGGVKLF 96  
 |||||  
 Db 89 TLVVQFTVKHEQNIDCGGVKLF 112  
 |||||  
 RESULT 6  
 Q91711 PRELIMINARY; PRT; 343 AA.  
 ID Q91711  
 AC Q91711;

DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE CALRETICULIN (FRAGMENT).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=93074997; PubMed=1445218;  
RA Treves S., Zorzato F., Pozzan T.;  
RT "Identification of calreticulin isoforms in the central nervous  
system.";  
RL Biochem. J. 287:579-581(1992).  
DR EMBL; X67598; CAA47867.1; -;  
DR InterPro: IP0001580; Calreticulin.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
FT NON\_TER 1  
FT TER 343  
FT SIGNAL 343  
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA3B91DE1 CRC64;  
  
Query Match 12.2%; Score 22; DB 13; Length 343;  
Best Local Similarity 100.0%; Pred. No. 1.7e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 151 FTHLYTLVLRPDNTYEVKIDNS 172  
Db 140 FTHLYTLVLRPDNTYEVKIDNS 161  
|||||  
RESULT 7  
ID Q91710 PRELIMINARY; PRT; 411 AA.  
AC Q91710;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE CALRETICULIN PRECUSOR (FRAGMENT).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=93074997; PubMed=1445218;  
RA Treves S., Zorzato F., Pozzan T.;  
RT "Identification of calreticulin isoforms in the central nervous  
system.";  
RL Biochem. J. 287:579-581(1992).  
DR EMBL; X67597; CAA47866.1; -;  
DR InterPro: IP0000886; ER.target.  
DR InterPro: IP0001580; Calreticulin.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 2.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
KW Signal.  
FT NON\_TER 1  
FT TER 12  
FT SIGNAL <1 12 POTENTIAL.

FT CHAIN 13 411 CALRETICULIN.  
SQ SEQUENCE 411 AA; 48344 MW; 891DA66E00EBBEFA CRC64;  
  
Query Match 12.2%; Score 22; DB 13; Length 411;  
Best Local Similarity 100.0%; Pred. No. 1.9e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 151 FTHLYTLVLRPDNTYEVKIDNS 172  
Db 163 FTHLYTLVLRPDNTYEVKIDNS 184  
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RESULT 8  
ID Q97372 PRELIMINARY; PRT; 387 AA.  
AC Q97372;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE CALRETICULIN PRECUSOR.  
OS Dirofilaria immitis.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Dirofilaria.  
OX NCBI\_TaxID=6287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99094497; PubMed=9879888;  
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;  
RT "Molecular characterization of a calcium-binding protein from the  
filarial parasite Dirofilaria immitis.";  
RL Mol. Biochem. Parasitol. 97:69-79(1998).  
DR EMBL; AF052978; AAD03405.1; -;  
DR InterPro: IP0001580; Calreticulin.  
DR Pfam: PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
KW Signal.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 387 CALRETICULIN.  
SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;  
  
Query Match 11.7%; Score 21; DB 5; Length 387;  
Best Local Similarity 100.0%; Pred. No. 2.3e-14;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 111 YNIMFGPDICGPGTKKVHVIF 131  
Db 126 YNIMFGPDICGPGTKKVHVIF 146  
|||||  
RESULT 9  
ID Q98984 PRELIMINARY; PRT; 419 AA.  
AC Q98984;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE CALRETICULIN.  
OS Rana rugosa (Frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
OX NCBI\_TaxID=8410;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96234004; PubMed=8654561;  
RA Yamamoto S., Nakamura M.;  
RT "Calnexin: its molecular cloning and expression in the liver of the  
frog, Rana rugosa.";

RL FEBS Lett. 387:27-32(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Yamamoto S.;

RT \*Strong expression of the calreticulin gene in the liver of Rana

RL J. Exp. Zool. 0:0-0(1996).

DR EMBL; D78589; BAA11425.1; -.

DR InterPro; IPR000886; ER\_target.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR PRODOM; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN\_1; 1.

DR PROSITE; PS00804; CALRETICULIN\_2; 1.

DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.

DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.

SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match

Best Local Similarity 11.1%; Score 20; DB 13; Length 419;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 HLYTLVPRDNTYEVKIDNS 172

|||||

DB 171 HLYTLVPRDNTYEVKIDNS 190

RESULT 10

O18478

ID O18478 PRELIMINARY; PRT; 375 AA.

AC O18478;

DT 01-JAN-1998 (TRENBLrel. 05, Created)

DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)

DE RAL-1 PROTEIN (FRAGMENT).

OS Litomosoides sigmodontis.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

OC Onchocercidae; Litomosoides.

OX NCBI\_TaxID-42156;

RN [1]

RP SEQUENCE FROM N.A.

RA MacLennan K., Hoffman W.H., Taylor D.W.;

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ001621; CAA04877.1; -.

DR InterPro; IPR001580; Calreticulin.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR PRODOM; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN\_1; 1.

DR PROSITE; PS00804; CALRETICULIN\_2; 1.

DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.

DR NON\_TER 375

SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match

Best Local Similarity 10.6%; Score 19; DB 5; Length 375;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKKVHVIF 131

|||||

DB 128 IMFGPDICGPGTKKVHVIF 146

RESULT 11

Q9U916

ID Q9U916 PRELIMINARY; PRT; 406 AA.

AC Q9U916;

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)

DE CALRETICULIN.

GN CRC OR CG9429.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID-7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-OREGON-R;

RA Dodo K., Sakoyama Y., Gamo S.;

RT \*Drosophila melanogaster calreticulin for mRNA.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB000718; BAA85379.1; -.

DR FLYBase; FBgn0005585; CRC.

DR InterPro; IPR001580; Calreticulin.

DR InterPro; IPR000886; ER\_target.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR PRODOM; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN\_1; 1.

DR PROSITE; PS00804; CALRETICULIN\_2; 1.

DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.

DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.

SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match

Best Local Similarity 10.6%; Score 19; DB 5; Length 406;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGPGTKKVHVIF 131

|||||

DB 130 IMFGPDICGPGTKKVHVIF 148

Search completed: January 14, 2002, 08:52:02

Job time: 113 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:34 ; Search time 83.2 Seconds  
(without alignments)  
160.255 Million cell updates/sec

Title: us-09-828-000-3

Perfect score: 971

Sequence: 1 EPAYVKEFLDGDGWTSRW.....PONTYEVKIDNSQVESGSLE 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*
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- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 971   | 100.0       | 180    | 21    | Human vasostatin ( |
| 2          | 971   | 100.0       | 400    | 21    | Recombinant human  |
| 3          | 971   | 100.0       | 417    | 10    | 60 kD Ro (Ro/SSA)  |
| 4          | 971   | 100.0       | 417    | 21    | Human MBP-calretic |
| 5          | 966   | 99.5        | 417    | 20    | Calreticulin. Hom  |
| 6          | 921   | 94.9        | 401    | 18    | Calreticulin. Hom  |
| 7          | 700   | 72.1        | 403    | 17    | Flea calreticulin  |
| 8          | 631   | 65.0        | 385    | 21    | Human secreted pro |
| 9          | 541.5 | 55.8        | 336    | 12    | Partial sequence o |
| 10         | 527   | 54.3        | 415    | 22    | Castor bean calret |
| 11         | 527   | 54.3        | 415    | 22    | Castor bean calret |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 12 | 510   | 52.5 | 421 | 21 | AAG24608 | Arabidopsis thalia |
| 13 | 510   | 52.5 | 421 | 21 | AAG47932 | Arabidopsis thalia |
| 14 | 510   | 52.5 | 424 | 21 | AAG24607 | Arabidopsis thalia |
| 15 | 510   | 52.5 | 424 | 21 | AAG47931 | Arabidopsis thalia |
| 16 | 510   | 52.5 | 441 | 21 | AAG30997 | Arabidopsis thalia |
| 17 | 510   | 52.5 | 444 | 21 | AAG30996 | Arabidopsis thalia |
| 18 | 327   | 33.7 | 61  | 21 | AA192352 | Recombinant human  |
| 19 | 318   | 32.7 | 60  | 21 | AA192354 | Recombinant human  |
| 20 | 318   | 32.7 | 280 | 21 | AA192355 | Recombinant delta- |
| 21 | 301.5 | 31.1 | 417 | 21 | AA177953 | A. thaliana enviro |
| 22 | 290   | 29.9 | 593 | 16 | AA171094 | Calnexin sequence. |
| 23 | 258   | 26.6 | 49  | 21 | AA192353 | Recombinant human  |
| 24 | 253   | 26.1 | 312 | 21 | AA192353 | Arabidopsis thalia |
| 25 | 253   | 26.1 | 312 | 21 | AAG47933 | Arabidopsis thalia |
| 26 | 253   | 26.1 | 332 | 21 | AAG30998 | Arabidopsis thalia |
| 27 | 250.5 | 25.8 | 84  | 21 | AAG41018 | Zea mays protein f |
| 28 | 238.5 | 24.6 | 530 | 21 | AAG26284 | Arabidopsis thalia |
| 29 | 238.5 | 24.6 | 530 | 21 | AAG46611 | Arabidopsis thalia |
| 30 | 238.5 | 24.6 | 567 | 21 | AAG46610 | Arabidopsis thalia |
| 31 | 227.5 | 23.4 | 542 | 22 | AAB66342 | Castor bean calnex |
| 32 | 200.5 | 20.6 | 532 | 21 | AAG04448 | Arabidopsis thalia |
| 33 | 200.5 | 20.6 | 548 | 21 | AAG04447 | Arabidopsis thalia |
| 34 | 190   | 19.6 | 122 | 20 | AA100924 | Human cClqR bindin |
| 35 | 190   | 19.6 | 122 | 20 | AA100925 | Rat cClqR binding  |
| 36 | 182   | 18.7 | 122 | 20 | AA100925 | Mouse cClqR bindin |
| 37 | 145   | 14.9 | 91  | 21 | AAG34014 | Arabidopsis thalia |
| 38 | 145   | 14.9 | 99  | 21 | AAG34013 | Arabidopsis thalia |
| 39 | 140.5 | 14.5 | 256 | 22 | AAB99168 | Human Endoplasmic  |
| 40 | 124.5 | 12.8 | 221 | 21 | AAB56468 | Human prostate can |
| 41 | 114.5 | 11.8 | 162 | 21 | AAG00147 | Human secreted pro |
| 42 | 114.5 | 11.8 | 162 | 21 | AAG00148 | Human secreted pro |
| 43 | 112.5 | 11.6 | 394 | 21 | AAG26285 | Arabidopsis thalia |
| 44 | 112.5 | 11.6 | 394 | 21 | AAG46612 | Arabidopsis thalia |
| 45 | 110.5 | 11.4 | 125 | 21 | AAG25999 | Zea mays protein f |

#### ALIGNMENTS

RESULT 1

AA192351

ID AA192351 standard; Protein; 180 AA.

AC AA192351;

DT 10-AUG-2000 (first entry)

XX Human vasostatin (calreticulin N-terminal 180 amino acids).

DE MBP-calreticulin; maltose binding protein; vasostatin; N-terminal; anglogenesis; inhibition; endothelial cell; anti-angiogenic; neuroprotective; antidiabetic; cytostatic; dermalogical; hepatic; immunosuppressive; antiinflammatory; anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.

OS Synthetic.

PN WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin.

PT useful for suppressing tumor growth  
 XX  
 PS  
 CC Claim 4; Page 82; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).

XX Sequence 180 AA;

Query Match 100.0%; Score 971; DB 21; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-99;  
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 E PAVYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60  
 DB 1 E PAVYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60  
 QY 61 SASFEPFNKQGLVVOFTVKHQNIDCGGYYVKLPNSLDQTDHMGDSYNTMFGPDIC 120  
 DB 61 SASFEPFNKQGLVVOFTVKHQNIDCGGYYVKLPNSLDQTDHMGDSYNTMFGPDIC 120  
 QY 121 GPCTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180  
 DB 121 GPCTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180

RESULT 2

AA92350  
 ID AAP92350 standard; Protein: 400 AA.

AC AAP92350;

XX 10-AUG-2000 (first entry)

DT Recombinant human MBP-calreticulin.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX N-PSDB; AAA09346, AAA09347.

XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 XX useful for suppressing tumor growth  
 PS  
 CC Claim 4; Page 80-81; 99pp; English.

XX Recombinant human MBP-calreticulin comprises the sequence of human  
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC Fragments of calreticulin causes at least 40% inhibition of  
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The  
 CC method may be used for inhibiting angiogenesis in a patient. The  
 CC angiogenesis is associated with a disease other than a tumor that is  
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental  
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,  
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).

XX Sequence 400 AA;

Query Match 100.0%; Score 971; DB 21; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-99;  
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 E PAVYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60  
 DB 1 E PAVYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60  
 QY 61 SASFEPFNKQGLVVOFTVKHQNIDCGGYYVKLPNSLDQTDHMGDSYNTMFGPDIC 120  
 DB 61 SASFEPFNKQGLVVOFTVKHQNIDCGGYYVKLPNSLDQTDHMGDSYNTMFGPDIC 120  
 QY 121 GPCTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180  
 DB 121 GPCTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180

RESULT 3

AA92276

ID AAP92276 standard; protein: 417 AA.

AC AAP92276;

XX 23-FEB-1990 (first entry)

XX 60 kD Ro (Ro/SSA) antigen.

XX Sjorens syndrome; systemic lupus erythematosus.

OS Synthetic.

XX WO8909273-A.

XX 05-OCT-1989.

XX 22-MAR-1989; 89WO-US01213.

XX 22-MAR-1988; 88US-0171634.

XX (TEXA ) UNIV OF TEXAS SYST.

XX Sontheimer RD, Capra JD, McCauliffe DP;

XX WPI; 1989-309537/42.

XX N-PSDB; AAP92276.

XX



PT DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen  
 PT - used in immunoassays to detect rheumatic disease  
 XX Disclosure; Fig 2; 88pp; English.  
 PS  
 CC Synthetic peptides corresp. to an epitopic core of Ro antigen are  
 CC expressed recombinantly to detect autoantibodies, for identification  
 CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,  
 CC or 241-255. The peptides may be substd. for ribonucleoprotein particle  
 CC antigens.  
 XX  
 SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 10; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-99;  
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDGLQTSQDARFYAL 60  
 DB 18 epavyfkeqfldgdgwtswieskhksdfgkflvssgkfygdeekdglqtsqdarfyal 77

QY 61 SASFEPSPNKGQTLVQVFTVKHEQNIDCGGYVKLPNSLDQTDHGDSEYNIMFGPDIC 120  
 DB 78 sasfepfsnkgqtlvqvftvkheqndicgggyvklfnsldqtdmhgdseynimfgpdic 137

QY 121 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 180  
 DB 138 gpgtkkvhvifnykgnvlinkdirckddeftthlytlivrpndtyevkidnsqvsagsle 197

RESULT 4  
 AAY92349  
 ID AAY92349 standard; Protein; 417 AA.  
 XX  
 AC AAY92349;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Human MBP-calreticulin.  
 XX  
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
 XX  
 OS Homo sapiens.  
 XX

Key Location/Qualifiers  
 FH Peptide 1..17  
 FT /label= signal\_peptide  
 FT Protein 18  
 FT /label= mature\_protein  
 XX  
 WO200020577-A1.  
 XX  
 PN  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-US23240.  
 XX  
 PR 06-OCT-1998; 98US-0103438.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Tosato G, Pike SE, Yao L;  
 PI WPI; 2000-303767/26.  
 XX  
 DR N-PSDB; AAA09346, AAA09347.  
 XX  
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth  
 XX  
 PS Disclosure; Page 79-80; 99pp; English.

XX  
 CC A novel method of inhibiting endothelial cell growth comprises  
 CC contacting the cells with calreticulin (or its fragments/variants).  
 CC fragments of calreticulin causes at least 40% inhibition of angiogenesis,  
 CC tumor growth and/or endothelial cell growth (claimed). The method may be  
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is  
 CC associated with a disease other than a tumor that is associated with  
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,  
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune  
 CC inflammation, atherosclerosis, excessive wound repair, retinal  
 CC neovascularization, macular degeneration, corneal graft rejection,  
 CC contact lens overwear, Crohn's disease, non-immune inflammation,  
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,  
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's  
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may  
 CC also be used for treating/inhibiting tumor growth especially  
 CC Kaposi's sarcoma (claimed).  
 XX  
 SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 21; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-99;  
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDGLQTSQDARFYAL 60  
 DB 18 epavyfkeqfldgdgwtswieskhksdfgkflvssgkfygdeekdglqtsqdarfyal 77

QY 61 SASFEPSPNKGQTLVQVFTVKHEQNIDCGGYVKLPNSLDQTDHGDSEYNIMFGPDIC 120  
 DB 78 sasfepfsnkgqtlvqvftvkheqndicgggyvklfnsldqtdmhgdseynimfgpdic 137

QY 121 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 180  
 DB 138 gpgtkkvhvifnykgnvlinkdirckddeftthlytlivrpndtyevkidnsqvsagsle 197

RESULT 5  
 AAY00927  
 ID AAY00927 standard; Protein; 417 AA.  
 XX  
 AC AAY00927;  
 XX  
 DT 28-MAY-1999 (first entry)  
 XX  
 DE Calreticulin.  
 XX  
 KW Clq and collectin receptor; cClqR binding domain; complement ubiquitin;  
 KW CUB functionality; inhibitor; complement activation; inflammation;  
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
 KW immune complex nephritis; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9907406-A1.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 12-AUG-1998; 98WO-GB02430.  
 XX  
 PR 12-AUG-1997; 97GB-0016998.  
 XX  
 XX (UYLE-) UNIV LEICESTER.  
 PA  
 XX Schwaebler W;  
 PI  
 XX WPI; 1999-180404/15.  
 DR  
 XX Use of a cClqR binding domain - to modulate complement ubiquitin  
 PT (CUB) functionality.  
 XX

PS Disclosure; Page 26-27; 31pp; English.

CC This sequence is calreticulin, a homologue of C1q and collectin receptor (cC1qR). The invention relates to the use of a cC1qR binding domain in a medicament to effect complement ubiquitin (CUB) functionality, and an inhibitor of the cC1qR binding domain in a medicament to inhibit CUB functionality. The cC1qR binding domain, or its inhibitor, can be used to treat a human or animal body. Particularly an inhibitor is used to treat complement activation involved in the initiation and maintenance of inflammation, for example in myocardial infarction, brain ischaemia (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus erythematosus, burns, immune complex nephritis, and to treat amyloid plaques in Alzheimer's disease. The use of cC1qR binding domain or inhibitor enables the CUB domain functionality to be modulated using a low molecular weight molecule.

XX Sequence 417 AA;

Query Match 99.5%; Score 966; DB 20; Length 417;  
Best Local Similarity 99.4%; Pred. No. 3.5e-98;  
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPAYVPEKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 60  
DB 18 epavytkeqfldgdgwtprwieskhksdfgkflvssgkfygdeekdkglqtsqdarfyal 77  
QY 61 SASPEFPSNKGQTLVQVFTVKHEQNIDCGGYVKLPFNSLDQTDHMGDSEYNTMFPGDIC 120  
DB 78 sasfepfsnkgqtlvvqftvkheqnidcggyvklfpnsldqtdmhgdseynlmfpgdic 137  
QY 121 GPCTKKVHVIFNYKGNVLINKDIRCKDDEFTHLVTPDNTYEVKIDNSQVESGSLE 180  
DB 138 gpgtkkvhvfnykgnvlinkdirckddeftthlylvprdpntyevkidnsqvesgsle 197

RESULT 6  
AAW11156  
ID AAW11156 standard; peptide; 401 AA.  
AC AAW11156;  
XX 31-MAY-1997 (first entry)  
XX Calreticulin.  
XX calreticulin; C-domain; restenosis; inhibitor.  
XX Homo sapiens.  
XX WO9636643-A1.  
XX 21-NOV-1996.  
XX 17-MAY-1996; 96WO-IB00471.  
XX 16-MAY-1996; 96US-0649417.  
XX 17-MAY-1995; 95US-0442844.  
XX (UYAL-) UNIV ALBERTA.  
XX Lucas A, Michalak M;  
XX WPI; 1997-012036/01.  
XX Inhibition of restenosis in patients - using calreticulin or a C-domain polypeptide of calreticulin or a variant with the same activity.  
XX Disclosure; Fig 1; 48pp; English.  
XX The present sequence is calreticulin. It and a C-domain derived peptide (AAW06736) are useful for treating a patient to inhibit restenosis. The

CC calreticulin-type cpds. are administered either parenterally,  
CC intravenously or via a catheter and can target areas of vascular damage  
CC to inhibit or prevent restenosis.

XX Sequence 401 AA;

Query Match 94.9%; Score 921; DB 18; Length 401;  
Best Local Similarity 95.0%; Pred. No. 3.1e-93;  
Matches 171; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 EPAYVPEKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 60  
DB 1 epvytkeqfldgdgwtprwieskhksdfgkflvssgkfygdeekdkglqtsqdarfyal 60  
QY 61 SASPEFPSNKGQTLVQVFTVKHEQNIDCGGYVKLPFNSLDQTDHMGDSEYNTMFPGDIC 120  
DB 61 sasfepfsnkgqtlvvqftvkheqnidcggyvklfpagldqkdmhgdsenlmfpgdic 120  
QY 121 GPCTKKVHVIFNYKGNVLINKDIRCKDDEFTHLVTPDNTYEVKIDNSQVESGSLE 180  
DB 121 gpgtkkvhvfnykgnvlinkdirckddeftthlylvprdpntyevkidnsqvesgsle 180

RESULT 7  
AAW04171  
ID AAW04171 standard; Protein; 403 AA.  
XX AAW04171;  
XX 12-DEC-1996 (first entry)  
XX Flea calreticulin PCTCal403.  
XX Calreticulin; flea; haematophagous insect; allergic dermatitis;  
XX vaccine; therapy; PCTCal403.  
XX Ctenocephalides felis.  
XX WO9628469-A1.  
XX 19-SEP-1996.  
XX 08-MAR-1996; 96WO-US03133.  
XX 09-MAR-1995; 95US-0401509.  
XX (HESK-) HESKA CORP.  
XX Rushlow KE, Stiegler GL;  
XX WPI; 1996-442861/44.  
XX N-PSDB; AAT39516;  
XX N-PSDB; AAT39517.  
XX Haematophagous insect calreticulin protein - used to reduce insect infestation and desensitise patients to allergic dermatitis  
XX Claim 5; Page 68-69; 86pp; English.  
XX Flea calreticulin protein PCTCal1589 (AAW04171) is a calcium-binding protein found in the salivary glands of Ctenocephalides felis.  
XX Its amino acid sequence was deduced from a cDNA clone (AAT39516) obtd. from a salivary gland cDNA library. Recombinant PCTCal1589 can be produced in host cells transformed with a vector carrying calreticulin nucleic acids. Calreticulin alters the blood feeding behaviour of haematophagous insects and can be administered to an animal to reduce infestation. It reduces calreticulin activity in insects, so reducing the insect burden on an animal. Calreticulin can be used to elicit an immune response, thereby desensitising an animal to allergic dermatitis caused by fleas, mosquitoes or Culicoides.

SQ Sequence 403 AA;

Query Match 72.1%; Score 700; DB 17; Length 403;  
 Best Local Similarity 71.7%; Pred. No. 7.8e-69;  
 Matches 129; Conservative 23; Mismatches 26; Indels 2; Gaps 2;

QY 2 PAVYFKEQFLDGGWTSRWIESKHK-SDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60  
 Db 19 pevlfleenfvd-dwtntwvseyhpqkefgkfvhtagkyndaeadkglqtgqdarfyal 77  
 QY 61 SASFEPFSGKQTLVYQFTVKHQNIDCGGGYVKLPNSLDQTDHMGDSYNTMFGPDIC 120  
 Db 78 shkfpsnkdktlvqfsvkhegnldcggylkgfsvnqkdmhgespyeimfgpdic 137  
 QY 121 GPCTKKVHVIENYKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180  
 Db 138 dbpttkkvhwifsykgnvlinkdirckddvrythvtytlvkvkpdnteyvlidnekvesgnle 197

RESULT 8  
 AAB32385  
 ID AAB32385 standard; Protein; 385 AA.  
 AC AAB32385;  
 DT 16-JAN-2001 (first entry)  
 DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:71.

Human; secreted protein; cytostatic; immunostimulant; antiproliferative;  
 cardiant; antiarrhythmic; antiviral; antibacterial; antifungal; cancer;  
 antiparasitic; neuroprotective; nootropic; antiinflammatory; anti-HIV;  
 antiangiogenic; antiarteriosclerotic; diagnosis; immune disorder; AIDS;  
 autoimmune disease; haematopoietic cell disorder; blood protein disorder;  
 agammaglobulinaemia; hyperproliferative disease; Gaucher's disease;  
 cardiovascular disorder; congenital heart defect; pulmonary atresia;  
 arrhythmia; ischaemia; angiogenesis related disorder; Crohn's disease;  
 atherosclerosis; neurological disease; Alzheimer's disease;  
 Huntington's; infectious disease; cat-scratch disease.

OS Homo sapiens.  
 XX  
 PN WO200047602-A1.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 08-FEB-2000; 2000WO-US03062.  
 XX  
 PR 10-FEB-1999; 99US-0119468.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM, Ebner R, Young PE, NI J, Soppet DR, Moore PA;  
 PI Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsoulis G;  
 XX  
 DR WPI: 2000-543578/49.  
 DR N-PSDB; AAC55204.  
 XX  
 PT New human nucleic acids encoding secreted proteins, useful in the  
 PT treatment, prevention or diagnosis of immune disorders (e.g. autoimmune  
 PT diseases), blood protein disorders and hyperproliferative diseases  
 PT (e.g. Gaucher's disease).  
 XX  
 PS Claim 11; Page 434-435; 488pp; English.  
 XX

The polynucleotide sequences given in AAC55190 to AAC55235 encode the  
 CC human secreted proteins given in AAB32371 to AAB32484. Human secreted  
 CC proteins have activities based on the tissues and cells the genes are  
 CC expressed in. Examples of activities include: cytostatic;  
 CC immunostimulant; antiproliferative; cardiant; antiarrhythmic; antiviral;  
 CC antibacterial; antifungal; antiparasitic; neuroprotective; nootropic;  
 CC antiinflammatory; antiangiogenic; anti-HIV; and antiarteriosclerotic. The

CC polynucleotides and polypeptides, or their agonists and antagonists, can  
 CC be used for treating, preventing or diagnosing immune disorders (e.g.  
 CC cancer, autoimmune diseases), disorders of haematopoietic cells, blood  
 CC protein disorders (e.g. agammaglobulinaemia), hyperproliferative  
 CC diseases (e.g. Gaucher's disease), cardiovascular disorders (e.g.  
 CC congenital heart defects, pulmonary atresia, arrhythmias, ischaemia),  
 CC angiogenesis related disorders (e.g. Crohn's disease, atherosclerosis),  
 CC neurological diseases (e.g. Alzheimer's disease, Huntington's chorea),  
 CC infectious diseases (e.g. AIDS, cat-scratch disease and other bacterial,  
 CC viral, parasitic or fungal diseases). AAC55181 to AAC55189 and AAB32370  
 CC represent sequences used in the exemplification of the present  
 CC invention.

SQ Sequence 385 AA;

Query Match 65.0%; Score 631; DB 21; Length 385;  
 Best Local Similarity 64.4%; Pred. No. 3e-61;  
 Matches 114; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 4 VYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYALSAS 63  
 Db 21 vyfkeefldghehwnrwlqstndsrfgfrlssgkfyghkekdkglqtqngryfalsar 80  
 QY 64 FEPFSGKQTLVYQFTVKHQNIDCGGGYVKLPNSLDQTDHMGDSYNTMFGPDICGPG 123  
 Db 81 fkpfsnkgktlvqytkvheqkmdcgggykvpadldqknlngksqyymfipdlogfd 140  
 QY 124 TKKVHVIENYKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180  
 Db 141 ikkvhvilhfknyhenkklirckvdfthlytlirpdisydvkldggsiesgsle 197

RESULT 9  
 AAR12312  
 ID AAR12312 standard; Protein; 336 AA.  
 XX AAR12312;  
 XX AC AAR12312;  
 DT 29-AUG-1991 (first entry)  
 XX  
 DE Partial sequence of Onchocera volvulus 42 kD antigen.  
 KW River blindness; onchocerciasis; vaccine; antigen; parasite.  
 XX Onchocerca volvulus.

| Key       | Location/Qualifiers  |
|-----------|----------------------|
| FT Region | 160..166             |
| FT        | /label= repeat unit  |
| FT        | /note= "hydrophilic" |
| FT Region | 177..183             |
| FT        | /label= repeat unit  |
| FT        | /note= "hydrophilic" |
| FT Region | 195..201             |
| FT        | /label= repeat unit  |
| FT        | /note= "hydrophilic" |

US5021342-A.

04-JUN-1991.

30-JUN-1988; 88US-0214264.

30-JUN-1988; 88US-0214264.

(UYHO-) UNIV HOSPITALS CLEV.

Greene BM, Unnasch TR;

WPI; 1991-185179/25.

N-PSDB; AAQ11987.

PT DNA encoding Onchocerca volvulus antigen - used to express  
 PT recombinant antigen for vaccine against onchocerciasis or river  
 blindness.

PS Disclosure; Fig 7; 20pp; English.

XX The sequence was deduced from a cDNA clone lambda RAL-1 prepd.  
 CC from RNA isolated from nodules excised from patients infected  
 CC with O. volvulus. The N-terminal is incomplete, however Abs  
 CC which specifically bind to protein prepd. from induced cultures  
 CC of lambda RAL-1 lysogens recognise a single polypeptide of mol.  
 CC wt. 42,000 in extracts of adult worms. Analysis deduced sequence  
 CC suggests that it encodes a protein of mol. wt. 39,130. If the  
 CC antigen is not subject to post-translational processing this  
 CC suggests that most of the coding sequence is present. The three  
 CC repeats are highly hydrophilic regions likely to be exposed on  
 CC the surface of the antigen and highly immunogenic. Recombinant  
 CC antigen expressed by the clone can be used stimulate T-cells of  
 CC individuals infected by the parasite to proliferate and may be  
 CC used as the basis for a vaccine against Onchocerciasis or river  
 blindness.

XX Sequence 336 AA;

Query Match 55.8%; Score 541.5; DB 12; Length 336;

Best Local Similarity 68.5%; Pred. No. 1.9e-51;

Matches 98; Conservative 21; Mismatches 23; Indels 1; Gaps 1;

QY 39 FYGDEKKGKGLQTSQDARYALSASF-PFSNKGOTLVVQFTVKHEQNIDCGGYYVKLFP 97

Db 1 fygdavkdqklttqdaakfyslgakfdksfnkgsalvqfsvkheqeidcggyvklma 60

QY 98 NSLDQTMHGDSEYNIMGPDICGPGTKKVVHVFYFNKGNVLINKDIRCKDDEFTHLTYL 157

Db 61 sdvnledshgetpyhmimgpdcpgptkvvhvfihykdrrnmhmkdkrckddvftthlyl 120

QY 158 IVRPONTYEVKIDNSQVESGSL 180

Db 121 lvsndtyevqldgkaesgele 143

RESULT 10

AAB66341

ID AAB66341 standard; Protein; 415 AA.

XX AAB66341;

DT 05-APR-2001 (first entry)

DE Castor bean calreticulin SEQ ID NO: 2.

KW Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;  
 KW calnexin; promoter; resistance.

XX Ricinus communis.

XX US6171864-B1.

PD 09-JAN-2001.

XX 05-JUL-1996; 96US-0675816.

PR 05-JUL-1996; 96US-0675816.

XX (PION-) PIONEER HI-BRED INT INC.

PI Coughlan SJ, Winfrey RJ;

XX WPI; 2001-122335/13.

DR N-PSDB; AAF29741, AAF29742.

PT New nucleic acid molecules encoding a calcium binding chaperone protein

PT in endoplasmic reticulum, calreticulin, and calreticulin promoter  
 PT sequences, useful for producing foreign gene products in plant cells  
 PS Claim 1; Fig 3; 45pp; English.

XX The present invention provides the protein and coding sequences for the  
 CC castor bean calreticulin protein and the calreticulin promoter sequence.  
 CC In addition, the castor bean calnexin protein, coding sequence and  
 CC promoter are also described. Calreticulin and calnexin are calcium  
 CC binding proteins found in the endoplasmic reticulum (er). The  
 CC calreticulin promoter sequence can be used in vectors to promote the  
 CC expression of foreign genes, particularly resistance genes, in plant  
 CC cells.

XX Sequence 415 AA;

Query Match 54.3%; Score 527; DB 22; Length 415;

Best Local Similarity 55.3%; Pred. No. 1e-49;

Matches 99; Conservative 31; Mismatches 43; Indels 6; Gaps 3;

QY 4 VYKEQFLDGDGWTSRWIESKHKSD---FGKFVLSGKFGYGDDEKDKGLQTSQDAREVAL 60

Db 22 vfeerf--edgwenrvwksdwkdkentagewnytsgkwngd-pndkgigtcsedyrfyai 78

QY 61 SASFEPFNNKGOTLVVQFTVKHEQNIDCGGYYVKLFPNSLDQTMHGDSEYNIMFGPDIC 120

Db 79 saefefsnkdkltlvqfsvkheqldcggymkllsstddqkkfggtpysimgpdc 138

QY 121 GPGTKKVVHVFYFNKGNVLINKDIRCKDDEFTHLTYLIVRPONTYEVKIDNSQVESGSL 179

Db 139 gystkvhailnyndtnhlikkevpcetdqlchvylvirpdatsillidnvektgsl 197

RESULT 11

AAB66343

ID AAB66343 standard; Protein; 415 AA.

XX AAB66343;

DT 05-APR-2001 (first entry)

DE Castor bean calreticulin.

KW Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;  
 KW calnexin; promoter; resistance.

XX Ricinus communis.

XX US6171864-B1.

PD 09-JAN-2001.

XX 05-JUL-1996; 96US-0675816.

PR 05-JUL-1996; 96US-0675816.

XX (PION-) PIONEER HI-BRED INT INC.

PI Coughlan SJ, Winfrey RJ;

XX WPI; 2001-122335/13.

DR N-PSDB; AAF29755.

XX New nucleic acid molecules encoding a calcium binding chaperone protein  
 PT in endoplasmic reticulum, calreticulin, and calreticulin promoter  
 PT sequences, useful for producing foreign gene products in plant cells  
 PS Disclosure; Fig 1B; 45pp; English.

XX The present invention provides the protein and coding sequences for the  
 CC castor bean calreticulin protein and the calreticulin promoter sequence.  
 CC In addition, the castor bean calnexin protein, coding sequence and

PR 14-MAY-1999; 9905-0134219.



PR 14-MAY-1999; 99US-0134219.  
 PR 14-MAY-1999; 99US-0134221.  
 PR 14-MAY-1999; 99US-0134370.  
 PR 18-MAY-1999; 99US-0134768.  
 PR 19-MAY-1999; 99US-0134941.  
 PR 20-MAY-1999; 99US-0135124.  
 PR 21-MAY-1999; 99US-0135353.  
 PR 24-MAY-1999; 99US-0135629.  
 PR 25-MAY-1999; 99US-0136021.  
 PR 27-MAY-1999; 99US-0136392.  
 PR 28-MAY-1999; 99US-0136782.  
 PR 01-JUN-1999; 99US-0137222.  
 PR 03-JUN-1999; 99US-0137528.  
 PR 04-JUN-1999; 99US-0137502.  
 PR 07-JUN-1999; 99US-0137724.  
 PR 08-JUN-1999; 99US-0138094.  
 PR 10-JUN-1999; 99US-0138540.  
 PR 10-JUN-1999; 99US-0138847.  
 PR 14-JUN-1999; 99US-0139119.  
 PR 16-JUN-1999; 99US-0139452.  
 PR 16-JUN-1999; 99US-0139453.  
 PR 17-JUN-1999; 99US-0139492.  
 PR 18-JUN-1999; 99US-0139454.  
 PR 18-JUN-1999; 99US-0139455.  
 PR 18-JUN-1999; 99US-0139456.  
 PR 18-JUN-1999; 99US-0139457.  
 PR 18-JUN-1999; 99US-0139458.  
 PR 18-JUN-1999; 99US-0139459.  
 PR 18-JUN-1999; 99US-0139460.  
 PR 18-JUN-1999; 99US-0139461.  
 PR 18-JUN-1999; 99US-0139462.  
 PR 18-JUN-1999; 99US-0139463.  
 PR 18-JUN-1999; 99US-0139750.  
 PR 18-JUN-1999; 99US-0139763.  
 PR 21-JUN-1999; 99US-0139817.  
 PR 22-JUN-1999; 99US-0139899.  
 PR 23-JUN-1999; 99US-0140353.  
 PR 23-JUN-1999; 99US-0140354.  
 PR 24-JUN-1999; 99US-0140695.  
 PR 28-JUN-1999; 99US-0140823.  
 PR 29-JUN-1999; 99US-0140991.  
 PR 30-JUN-1999; 99US-0141287.  
 PR 01-JUL-1999; 99US-0141842.  
 PR 01-JUL-1999; 99US-0142154.  
 PR 02-JUL-1999; 99US-0142055.  
 PR 06-JUL-1999; 99US-0142390.  
 PR 08-JUL-1999; 99US-0142803.  
 PR 09-JUL-1999; 99US-0142920.  
 PR 12-JUL-1999; 99US-0142977.  
 PR 13-JUL-1999; 99US-0143542.  
 PR 14-JUL-1999; 99US-0143624.  
 PR 15-JUL-1999; 99US-0144005.  
 PR 16-JUL-1999; 99US-0144085.  
 PR 16-JUL-1999; 99US-0144086.  
 PR 19-JUL-1999; 99US-0144325.  
 PR 19-JUL-1999; 99US-0144331.  
 PR 19-JUL-1999; 99US-0144332.  
 PR 19-JUL-1999; 99US-0144333.  
 PR 19-JUL-1999; 99US-0144334.  
 PR 19-JUL-1999; 99US-0144335.  
 PR 20-JUL-1999; 99US-0144352.  
 PR 20-JUL-1999; 99US-0144632.  
 PR 20-JUL-1999; 99US-0144884.  
 PR 21-JUL-1999; 99US-0144814.  
 PR 21-JUL-1999; 99US-0145086.  
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OM protein - protein search, using sw model

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ALIGNMENTS

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; Patent No. 6171864  
; GENERAL INFORMATION:  
; APPLICANT: Coughlan, Sean J.  
; APPLICANT: Winfrey, Jr., Ron J.  
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 701 Fifth Ave. Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/675,816  
; FILING DATE: 05-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NO. 6171864tenburg, Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 750027.401  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206-622-4900  
; TELEFAX: (206)-682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
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; MOLECULE TYPE: protein  
US-08-675-816-2

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; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuo
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; TITLE OF INVENTION: PROTEIN PRODUCTION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296.362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
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; MOLECULE TYPE: protein
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QY 53 QDAREYALSASF-EPPFSNKGOTLVVQFTVKHEQNTDCGGYVYKLFPPN-----SLDQTDHMG 107
Db 125 SRAKHHAISAKLNKPFLLFTDKPLVQYEVFNFGIECGGAYVYKLLSKTPELNLDQ--PHD 182
QY 108 DSEYNIMFGPDICGPGTKVHVIFNFKGNVLYNKDKDDEFTHLTYLVRPNTYEVKIDNSQ 157
Db 183 KPTYITMFGPDICGGE--DYKLFHIFRHKPKTGVYEEKHAKRPDADLKTYFTDKKTHLYTL 241
QY 158 IVRPONTYEVKIDNSQVSGSL 179
Db 242 ILNPNSEFELVDQSIIVNSGNL 263
```

```

RESULT 3
US-08-675-816-6
; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675.816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 542 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-6

Query Match 23.4%; Score 227.5; DB 4; Length 542;
Best Local Similarity 36.0%; Pred. No. 2.2e-17;
Matches 64; Conservative 24; Mismatches 73; Indels 17; Gaps 10;

QY 6 FKEQFLDGCWTSRWIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDAREYALSASF- 64
Db 35 FYESEF--EDSFEGRWTLA-KDDY-KGEWKHAKSEGHDE--YGLLVSEKARKYAIVKELD 88
QY 65 EPPFSNKGOTLVVQFTVKHEQNTDCGGYVYK-LFPNSLDQT--DMHGDSEYNIMFGPDICG 121
Db 89 EPATLKDGTIVLQFETRFQNGIECGGAYLYKLPQEGWTPKDFDNDSPSYIMFGPDICG 148
QY 122 PGTKVHVIFNFKG--KNVLYNKDIR----CKDDEFTHLTYLVRPNTYEVKIDNSQ 173
Db 149 -ATNKVHFILKHKPKSGYIEHHLKYPSPVSDKLTHVYTAILKPDNELRLIVDGE 205

RESULT 4
US-09-181-706-8
; Sequence 8, Application US/09181706
; Patent No. 6130068
; GENERAL INFORMATION:
; APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
; APPLICANT: Robert F. Dubose, Richard S. Johnson
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
```

Query Match 9.2%; Score 89; DB 4; Length 650;  
Best Local Similarity 20.6%; Pred. No. 0.14;  
Matches 41; Conservative 25; Mismatches 91; Gaps 6;  
Indels 42; Gaps 6;

|  |    |     |   |     |
|--|----|-----|---|-----|
|  | QY | 62  | ASPEPSNKGQTILVQFTVKHEQNIDCGGGYKVLFPNSLDQDTMHGDSEYNFMFGPDICG | 121 |
|  |    |     |   |     |
|  | Dδ | 507 | DS--PYSGALCTYSMAIKHFSFKLGGYTKQLPSP-----APGICL               | 548 |
|  |    |     |   |     |
|  | QY | 122 | PGFKKY-HVFN-----YKGKNVLINKDIRCKDDETHLYTLIVRP                | 161 |
|  |    |     |   |     |
|  | Dδ | 549 | PACKVVPHITFDIEQYNELDLIIKLQPIFEGPGSVAKWDIKEKEHREHYRIFKE      | 608 |
|  |    |     |   |     |
|  | QY | 162 | DNTYEYKIDNSQVESGSLE   | 180 |
|  |    |     |   |     |
|  | Dδ | 609 | NTIYSFDTKSKQTRSAQVD   | 627 |

```

RESULT      6
US-09-459-066-8
; Sequence 8, Application US/09459066
; Patent No. 6187909
;
GENERAL INFORMATION:
; APPLICANT: Striggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
;
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a

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CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459,066  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: 08/958,598  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)470-4189  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 660 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-459-066-8

Query Match 9.2%; Score 89; DB 4; Length 660;  
Best Local Similarity 20.6%; Pred. No. 0.14;  
Matches 41; Conservative 25; Mismatches 91; Indels 42; Gaps 6;  
QY 5 YFKEQFLDGGQWTSRWTESKHKSDFGKFLVS---SGKFYGDDEKDKGLQTSQDARFYALS 61  
DB 448 YIAQCLNDEGGPSS-ISSRNWSTFLKVECDIDGRSQRQIHSKAIKATNDNTILYVFF 506  
QY 62 ASFPFPFNKGQTLVYQFTVXHEQVYKLFPPNSLDQTDHMGDSEYNIMFGPDICG 121  
DB 507 DS--PYSKSALCTYSMAIKHSFSTSLGGVTKQLPSP-----APGICL 548  
QY 122 PGTKKV-HVTFN-----YKKNVLINKDICKDDETHLYTLVRP 161  
DB 549 PAGVVPHTTFDIEQYNELDDIITKLPSQIFPGSGVKWFDIKEKEHREYRIYFIKE 608  
QY 162 DNTVEVKIDNSQVESGSL 180  
DB 609 NTIYFDTKSKQTRSAQVD 627

RESULT 7  
US-08-245-511-48  
Sequence 48, Application US/08245511  
Patent No. 5985900  
GENERAL INFORMATION:  
APPLICANT: Masure, H Robert  
APPLICANT: Pearce, Barbara J  
APPLICANT: Tuomanen, Elaine  
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND  
CELLULAR VACCINES BASED THEREON  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/245,511  
FILING DATE: 18-MAY-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/116,541

FILING DATE: 01-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-069 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 642 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pneumoniae  
IMMEDIATE SOURCE:  
CLONE: amia  
FEATURE:  
OTHER INFORMATION: NOTE: the reference contains a  
OTHER INFORMATION: sequence error; the correct sequence shown below is obtain  
OTHER INFORMATION: from GENBANK  
PUBLICATION INFORMATION:  
AUTHORS: Allouing, et al.  
JOURNAL: Mol. Microbiol.  
VOLUME: 4  
PAGES: 633-644  
DATE: 1990  
US-08-245-511-48

Query Match 8.0%; Score 77.5; DB 2; Length 642;  
Best Local Similarity 21.2%; Pred. No. 2.6;  
Matches 42; Conservative 20; Mismatches 81; Indels 55; Gaps 8;  
QY 16 WTSP-----W-----TESKHSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYALSASF 64  
DB 164 WNSKLTYSIFWPLNEEFETSKGSDFAKPTDPTSLLYNGPFLKGLTAKSSVEF-----VKN 219  
QY 65 EPPFNKGQTLVYQFTVKH-----EQNIDCGG-GYVKLFPPNSLDQTDHMGDSEY 111  
DB 220 EQYWDKENVHLDITNLAYYDGSQDQESLERNFTSGAYSARLYPTSSNYKVAEYKDIY 279  
QY 112 NIMFGPDICGPTKKVHVIFYK-----KNVLINKDIR----- 145  
DB 280 YTQSGSGIAGLGVNIDRQSYNTSKTTDSEKVAATKALLNKDFRQALNFALDRSAYSQAI 339  
QY 146 -CKDDETHLYTLVRPD 162  
DB 340 NGKDGALAVRNLFVKPD 357  
RESULT 8  
US-08-600-993A-48  
Sequence 48, Application US/08600993A  
Patent No. 5981229  
GENERAL INFORMATION:  
APPLICANT: Masure, H Robert  
APPLICANT: Pearce, Barbara J  
APPLICANT: Tuomanen, Elaine  
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND  
CELLULAR VACCINES BASED THEREON  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601



```

; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Mitcham, Jennifer L.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND IMMUNODIAGNOSIS OF PROSTATE CANCER
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,026
; FILING DATE: 07-OCT-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-946-026-53

Query Match 7.9%; Score 77; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 14; Conservative 0; Mismatches 0; Indels

QY 2 PAVYFKEQFLDGDG 15
Db 2 PAVYFKEQFLDGDG 15

RESULT 10
US-08-991-408-4
; Sequence 4, Application US/08991408
; Patent No. 6008017
; GENERAL INFORMATION:
; APPLICANT: ARLETH, ANTHONY J.
; APPLICANT: WILLETE, ROBERT N.
; APPLICANT: ELSHOURBAGY, NABIL A.
; APPLICANT: LI, XIAOTONG
; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSQ for Windows Version 2.0

```



QY 126 KHVIFNYKGNVLI--NKDIRCKDDETHLYTLVLRPONTYEVK 168  
Db 973 EIYSI-----GDSVLIHFHTDDTINKKGFIHYKSIKIRYPTDTHTKK 1013

## RESULT 13

US-08-991-408-2  
; Sequence 2, Application US/08991408  
; Patent No. 6008017  
; GENERAL INFORMATION:  
; APPLICANT: ARLETH, ANTHONY J.  
; APPLICANT: WILLETTTE, ROBERT N.  
; APPLICANT: ELSHOURBAGY, NABIL A.  
; APPLICANT: LI, XIAOFONG  
; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,408  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/034,471  
; FILING DATE: 02-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: ATG-50038  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1013 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-991-408-2

Query Match 7.7%; Score 75; DB 3; Length 1013;  
Best Local Similarity 31.4%; Pred. No. 9.7;  
Matches 33; Conservative 15; Mismatches 39; Indels 18; Gaps 7;

QY 68 SNKGQTLVVOF-TVKHEQNIDCGGVYKLPNLSLDQTDMDHGDSEYNIMFGPDTCGPG-TK 125  
Db 923 SERGSRLEISFQFEVEEADCGYDYVELF-DGLDSTAV-GLGRF-----CGSGPPE 972

QY 126 KHVIFNYKGNVLI--NKDIRCKDDETHLYTLVLRPONTYEVK 168  
Db 973 EIYSI-----GDSVLIHFHTDDTINKKGFIHYKSIKIRYPTDTHTKK 1013

## RESULT 14

US-09-240-473-5  
; Sequence 5, Application US/09240473  
; Patent No. 6297011  
; GENERAL INFORMATION:  
; APPLICANT: Greenspan, Daniel S

; APPLICANT: Takahara, Kazuhiko  
; APPLICANT: Hoffman, Guy G  
; TITLE OF INVENTION: Mammalian Tolloid-Like Protein  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53703  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/240,473  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berson, Bennett J  
; REGISTRATION NUMBER: 37094  
; REFERENCE/DOCKET NUMBER: 960296.93839  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608-251-5000  
; TELEFAX: 608-251-9166  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1013 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-240-473-5

Query Match 7.7%; Score 75; DB 4; Length 1013;  
Best Local Similarity 31.4%; Pred. No. 9.7;  
Matches 33; Conservative 15; Mismatches 39; Indels 18; Gaps 7;

QY 68 SNKGQTLVVOF-TVKHEQNIDCGGVYKLPNLSLDQTDMDHGDSEYNIMFGPDTCGPG-TK 125  
Db 923 SERGSRLEISFQFEVEEADCGYDYVELF-DGLDSTAV-GLGRF-----CGSGPPE 972

QY 126 KHVIFNYKGNVLI--NKDIRCKDDETHLYTLVLRPONTYEVK 168  
Db 973 EIYSI-----GDSVLIHFHTDDTINKKGFIHYKSIKIRYPTDTHTKK 1013

## RESULT 15

US-08-231-193A-56  
; Sequence 56, Application US/08231193A  
; Patent No. 5849895  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrrie P.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lu, Chin-Chun

; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
; TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231.193A
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,459
; FILING DATE: 20-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1484 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-193A-56

Query Match
Best Local Similarity 7.5%; Score 72.5; DB 2; Length 1484;
Matches 23; Conservative 13; Mismatches 28; Indels 19; Gaps 4;

QY 45 KDKG--LQTSQDARYALASAPFSPNKGQTLVQFTVKHEQNIDCGGYV---KLFPS 99
    ||| : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1325 KDKGRFMDGSPYAHMFENSAGESTEFANKSSVP---TAGHHHHNNPGGGYMLSKSLYPD 1381
    ||| : | : | : | : | : | : | : | : | : | : | : | : | :

QY 100 L-----DQTDHMGDSEY 111
    : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1382 VTQNPFIPTFGDDQCLLHGSKSY 1404
    : | : | : | : | : | : | : | : | : | : | : | : | :

```

Search completed: January 9, 2002, 14:59:42  
Job time: 69 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:53 ; Search time 43.73 Seconds  
(without alignments)  
313.547 Million cell updates/sec

Title: US-09-828-000-3

Perfect score: 971  
Sequence: 1 EPAVYFKEQFLDGDGWTSRW.....PDNTYEVKIDNSQVESGSLE 180

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 971   | 100.0       | 417    | 1 A37047 | calreticulin precu |
| 2          | 933   | 96.1        | 416    | 2 JH0819 | calreticulin precu |
| 3          | 931   | 95.9        | 418    | 1 A34154 | calreticulin precu |
| 4          | 930   | 95.8        | 400    | 2 S43376 | calreticulin, brai |
| 5          | 930   | 95.8        | 416    | 1 S06763 | calreticulin precu |
| 6          | 835   | 86.0        | 411    | 2 S29129 | calreticulin precu |
| 7          | 804   | 82.8        | 405    | 1 JH0795 | calreticulin precu |
| 8          | 797   | 82.1        | 384    | 2 S29130 | calreticulin (clon |
| 9          | 796   | 82.0        | 419    | 2 S71343 | calreticulin precu |
| 10         | 699   | 72.0        | 406    | 2 A56637 | calreticulin homol |
| 11         | 619.5 | 63.8        | 395    | 2 S25851 | calreticulin precu |
| 12         | 542.5 | 55.9        | 336    | 2 A32507 | 41K larval antigen |
| 13         | 539   | 55.5        | 412    | 2 T05703 | calreticulin - bar |
| 14         | 539   | 55.5        | 415    | 2 T05705 | calreticulin - bar |
| 15         | 536   | 55.2        | 421    | 2 S58170 | calreticulin precu |
| 16         | 531   | 54.7        | 416    | 2 T14554 | calreticulin - bee |
| 17         | 527   | 54.3        | 415    | 2 T10172 | calreticulin - cas |
| 18         | 522.5 | 53.8        | 421    | 2 S36799 | calreticulin precu |
| 19         | 522   | 53.8        | 416    | 2 T15968 | calreticulin call  |
| 20         | 517   | 53.2        | 389    | 2 T03691 | calreticulin - com |
| 21         | 512   | 52.7        | 425    | 2 C96605 | calreticulin (Crt) |
| 22         | 510   | 52.5        | 444    | 2 H86224 | hypothetical prot  |
| 23         | 496   | 51.1        | 393    | 1 A48573 | calreticulin autoa |
| 24         | 347   | 35.7        | 422    | 2 T07841 | probable calreticu |
| 25         | 293   | 30.2        | 591    | 2 B54354 | calnexin precursor |
| 26         | 290   | 29.9        | 591    | 2 C54354 | calnexin precursor |
| 27         | 290   | 29.9        | 592    | 2 I53260 | calnexin - human   |
| 28         | 290   | 29.9        | 593    | 1 A37273 | calnexin precursor |
| 29         | 288   | 29.7        | 592    | 2 A46673 | calnexin precursor |

## ALIGNMENTS

```

RESULT      1
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
C:Accession: A42330; A37047; A46452; A28812; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t
A:Reference number: A42330; MUID:92129342
A:Accession: A42330
A:Molecule type: DNA
A:Residues: 1-417 <MC2>
A>Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)
R:McCaulliffe, D.P.; Lux, P.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
A:Reference number: A37047; MUID:90237213
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MCC>
A:Cross-references: GB:M32294; NID:G37486; PIDN:AAA36582.1; PID:G337487
R:Rothead, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <R0K>
A:Cross-references: GB:M84739; NID:G179881; PIDN:AAA51916.1; PID:G179882
A>Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence
A:Reference number: A28812; MUID:88273610
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A>Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
A:Reference number: PH1525; MUID:93115648
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Rojsiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

```

A:Reference number: A40346; MUID:92002034  
A:Accession: A40346  
A:Molecule type: protein  
A:Residues: 18-34, 'R' <RO>  
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.  
Biochem. J. 270, 545-548, 1990  
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the Golgi apparatus  
A:Reference number: S11475; MUID:90380058  
A:Accession: S11475  
A:Molecule type: protein  
A:Residues: 18-32 <KRA>  
R:Lamerdin, J.; McCreedy, P.; Stillwagen, S.; Ramirez, M.; Carrano, A.  
submitted to the EMBL Data Library, November 1996  
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region on human chromosome 17p11.2  
A:Reference number: 222906  
A:Accession: T45075  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-417 <LAM>  
A:Cross-references: EMBL:AD000092; PIDN:AA851176.1  
A:Experimental source: cell line 5HL2-B; fibroblast  
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and Sjogren's syndrome  
C:Genetics:  
A:Gene: GDB:CALR  
A:Cross-references: GDB:125179; OMIM:109091  
A:Map position: 19p13.3-19p13.2  
A:Introns: 31/1; 65/1; 133/1; 164/3; 272/3; 320/3; 351/3  
A:Note: CRTC  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; integrin binding  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-417/Product: calreticulin #status predicted <MAT>  
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 971; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 3.3e-80;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPAYFKQFLDGDGWTNRWIESKHSKSDFGKFLVSSGKFGYDGEKDKGLQTSQDARFYAL 60  
Db 18 EPAYFKQFLDGDGWTNRWIESKHSKSDFGKFLVSSGKFGYDGEKDKGLQTSQDARFYAL 77

Qy 61 SASPEFFNKGQTLVQVTVKHEQIDCGGVKFLFNSLDQTMHGDSEYNMFDPIC 120  
Db 78 SASPEFFNKGQTLVQVTVKHEQIDCGGVKFLFNSLDQTMHGDSEYNMFDPIC 137

Qy 121 GPGTKKHVIFNKGKLVINKIDCKDDETHLYTLVRPNTVEYKIDNSQVSGSLE 180  
Db 138 GPGTKKHVIFNKGKLVINKIDCKDDETHLYTLVRPNTVEYKIDNSQVSGSLE 197

RESULT 2  
JH0819  
Calreticulin precursor - rat  
N:Alternata names: calcium-binding protein 3  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text change 20-Jun-2000  
C:Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045  
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamamoto, T.; Arai, K.; Okinaga, S.  
Exp. Cell Res. 205, 101-110, 1993  
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome  
A:Reference number: A49176; MUID:93202172  
A:Accession: JH0819  
A:Molecule type: mRNA  
A:Residues: 1-416 <NAK>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA411345.1; PID:g1845572  
A:Accession: A49176  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-416 <NA2>  
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA411345.1; PID:g1845572  
A:Experimental source: Sprague-Dawley, spermatogenic cells

A:Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBIPI:127643)  
R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel  
Nucleic Acids Res. 18, 4933, 1990  
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerca volvulus calreticulin  
A:Reference number: S11205; MUID:90370496  
A:Accession: S11205  
A:Molecule type: mRNA  
A:Residues: 1-416 <MUR>  
A:Cross-references: EMBL:X53363; NID:955854; PIDN:CAA37446.1; PID:g55855  
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.  
Biochem. Biophys. Res. Commun. 186, 668-673, 1992  
A:Title: Calreticulin is present in the acrosome of spermatids of rat testis.  
A:Reference number: PC1109; MUID:92360010  
A:Accession: PC1109  
A:Molecule type: protein  
A:Residues: 18-32 <NAK2>  
A:Experimental source: testis, strain Sprague-Dawley  
R:Soennichsen, B.; Fueillekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mies  
submitted to the EMBL Data Library, May 1994  
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticulin in the ER  
A:Reference number: S45036  
A:Accession: S45036  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-416 <SOE>  
A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841  
R:Lone, Y.C.; Bailly, A.; Latruffe, N.  
submitted to the EMBL Data Library, December 1988  
A:Reference number: S04867  
A:Accession: S04867  
A:Molecule type: mRNA  
A:Residues: 'R', 270-358, 'AAG' <LON>  
A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930360  
A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase  
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kametaki, T.  
Biochim. Biophys. Acta 1158, 339-344, 1993  
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmunoantigenic proteins in rat liver vesicles  
A:Reference number: S39371; MUID:94072621  
A:Accession: S39372  
A:Molecule type: protein  
A:Residues: 18-23, 'X', 25-32 <YOK>  
R:Van, P.N.; Peter, F.; Soelling, H.D.  
J. Biol. Chem. 264, 17494-17501, 1989  
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes  
A:Reference number: A34473; MUID:90008920  
A:Accession: A34473  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-36 <VAN>  
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M  
Biochem. J. 271, 473-480, 1990  
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage vesicles  
A:Reference number: S13045; MUID:91054414  
A:Accession: S13045  
A:Molecule type: protein  
A:Residues: 18-29 <TRE>  
C:Superfamily: calreticulin  
C:Keywords: calcium binding; glycoprotein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-416/Product: calreticulin #status experimental <MAT>  
F:204-212/Region: nuclear location signal  
F:413-416/Region: nuclear retention signal  
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.1%; Score 933; DB 2; Length 416;  
Best Local Similarity 94.4%; Pred. No. 8.8e-77;  
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EPAYFKQFLDGDGWTNRWIESKHSKSDFGKFLVSSGKFGYDGEKDKGLQTSQDARFYAL 60  
Db 18 DPATYFKQFLDGDGWTNRWIESKHSKSDFGKFLVSSGKFGYDGEKDKGLQTSQDARFYAL 77

**Query**

61 SASPEPSNKGQTLVVOFTVKHEQNIDCGGYVKLFNPNSLDQTDMHGDSYNTMFGPDIC 120  
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**Qy** 121 GPGTKKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEYKIDNSOVESGSL 180  
II | |||||  
**Db** 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEYKIDNSOVESGSL 197  
II | |||||

**RESULT 3**

A34154  
calreticulin precursor, skeletal muscle - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A34154; S13047  
R:Filiegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.  
J. Biol. Chem. 264, 21522-21528, 1989  
A:title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) c  
A:Reference number: A34154; MUID:90094320  
A:Accession: A34154  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-418 <P>  
A:CROSS-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164859  
R:Reves, S.; de Mattei, M.; Ianfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld  
Biochem. J. 271, 473-480, 1990  
A:title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
A:Reference number: S13045; MUID:91054414  
A:Accession: S13047  
A:Molecule type: protein  
A:Residues: 19-32 <TRE>  
C:Superfamily: calreticulin  
C:Keywords: skeletal muscle  
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F:415-418/Region: endoplasmic reticulum retention signal

**Query Match**      95.9%; Score 931; DB 1; Length 418;  
**Best Local Similarity** 95.6%; Pred. NO. 1.3e-76;  
**Matches** 172; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

**Qy** 1 EPAYFYKEQLDGDGTWRWIESKHKSDFGVLSGSKFYGDEKDGLQTSODARFYAL 60  
II | |||||  
**Db** 18 EPVVFYKEQLDGDGTWRWIESKHKSDFGVLSGSKFYGDEKDGLQTSODARFYAL 77  
II | |||||  
**Qy** 61 SASPEPSNKGQTLVVOFTVKHEQNIDCGGYVKLFNPNSLDQTDMHGDSYNTMFGPDIC 120  
II | |||||  
**Db** 78 SARFEPSSNGQPLVVQFTVKHEQNIDCGGYVKLPAGLDQDKMDHGDSEYNIMFGPDIC 137  
II | |||||  
**Qy** 121 GPGTKKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEYKIDNSOVESGSL 180  
II | |||||  
**Db** 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEYKIDNSOVESGSL 197  
II | |||||

**RESULT 4**

S43376  
calreticulin, brain isoform 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:date: 20-Oct-1994 #sequence\_revision 23-Mar-1995 #text\_change 07-May-1999  
C:Accession: S43376; S36801  
R:Matsuoka, K.; Seto, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.  
Biochem. J. 298, 435-442, 1994  
A:title: Covalent structure of bovine brain calreticulin.  
A:Reference number: S43376; MUID:94183174  
A:Accession: S43376  
A:Molecule type: protein  
A:Residues: 1-400 <MAT>  
A:Experimental source: brain  
R:Liu, N.; Fine, R.E.; Johnson, R.J.  
Biochim. Biophys. Acta 1202, 70-76, 1993  
A:title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.  
A:Reference number: S36799; MUID:93385184









Query Match 55.2%; Score 536; DB 2; Length 421;  
Best Local Similarity 56.4%; Pred. No. 6.7e-41;  
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;  
QY 4 VYFKEQFLDGDGWTSRWIESKHSD--FGKFVLSGKFGYDEEKDKGLOTSDAREYAL 60  
DB 27 VYFQKEF--EDGWESRWKSEWKKDENMAGENHTSGKNGDAE-DKGIOTSEYRFYAI 83  
QY 61 SASFEPFSNKGOTLVVQFTVKHEQNIDCGGGYVKLFNSLDQTDHMGDSEYNIMFGPDIC 120  
DB 84 SAEPPEFSNKKDTLVLFQFSVKEQKLDGCGGYVKLLGGVDVQKKFGGDTSYSIMFGPDIC 143  
QY 121 GPGTKKVVHVFNYKGNVLINKDIRCKDDEFTHLVTLIVRPDNTYEVKIDNSQVESGSL 179  
DB 144 GYSTKKVHTTLTKDGNHLLIKDVPCETDQLTHVYTLIIRPDATYSILIDNEEKQTGSI 202

Search completed: January 9, 2002, 15:02:02  
Job time: 189 sec





cells.";  
RL Biochem. J. 270:545-548(1990).  
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RN SEQUENCE OF 18-28.  
RC TISSUE=Liver;  
RX MEDLINE=93162045; PubMed=1286669;  
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
Pascual C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,  
Appel R.D., Hughes G.J.;  
RT Human liver protein map: a reference database established by  
microsequencing and gel comparison.";  
RT Electrophoresis 13:992-1001(1992).  
[8]  
RN PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.  
RC TISSUE=Keratinocytes;  
RX MEDLINE=93162043; PubMed=1286667;  
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Cells J.E.,  
Vandekerckhove J.;  
RT Microsequences of 145 proteins recorded in the two-dimensional gel  
protein database of normal human epidermal keratinocytes.";  
RL Electrophoresis 13:960-969(1992).  
[9]  
RN SEQUENCE OF 18-26.  
RC TISSUE=Colon carcinoma;  
RX MEDLINE=97795306; PubMed=9150948;  
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
RT A two-dimensional gel database of human colon carcinoma proteins.";  
RL Electrophoresis 18:605-613(1997).  
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
CC -1- LOW AFFINITY CALCIUM-BINDING SITES.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -1- CAUTION: WAS ORIGINALLY (REF. 2) THOUGHT TO BE THE RO AUTOANTIGEN.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL; M84739; AAA51916.1; -;  
DR EMBL; M32294; AAA36582.1; -;  
DR EMBL; AD000092; AAB51176.1; -;  
DR PIR; A37047; A37047.  
DR PIR; S11475; S11475.  
DR PIR; A42330; A42330.  
DR PIR; A46452; A46452.  
DR SWISS-2DPAGE; P27797; HUMAN.  
DR Aarbus/Ghent-2DPAGE; 9401; IEF.  
DR HSC-2DPAGE; P27797; HUMAN.  
DR MIM; 109091; -;  
DR InterPro; IPR001580; Calreticulin.  
DR InterPro; IPR000886; ER target.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00636; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00014; ER-TARGET; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 417 CALRETICULIN.  
FT DOMAIN 18 197 N-DOMAIN.  
FT DOMAIN 198 308 P-DOMAIN.  
FT DOMAIN 309 417 C-DOMAIN.  
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.  
FT REPEAT 191 202 1-1.  
FT REPEAT 210 221 1-2.  
FT REPEAT 227 238 1-3.

FT REPEAT 244 255 1-4.  
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.  
FT REPEAT 259 269 2-1.  
FT REPEAT 273 283 2-2.  
FT REPEAT 287 297 2-3.  
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.  
FT DISULFID 137 163 BY SIMILARITY.  
FT SITE 414 417 PREVENT SECRETION FROM ER.  
FT CONFLICT 35 35 MISSING (IN REF. 3).  
SQ SEQUENCE 417 AA: 48141 MW: 637330 Cys1054Fb2 CRC64;  
  
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Best Local Similarity 100.0%; Pred. No. 4.8e-80;  
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EPAVYKQFLDGDGWTGWSRWIESKHSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60  
Db 18 EPAVYKQFLDGDGWTGWSRWIESKHSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 77  
QY 61 SASFEPFSNKGOTLVVQFTVKHEQNDICGGYVKKLPPNSLDQTDHMGDSEYNTMFGPDIC 120  
Db 78 SASFEPFSNKGOTLVVQFTVKHEQNDICGGYVKKLPPNSLDQTDHMGDSEYNTMFGPDIC 137  
QY 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 180  
Db 138 GPGTKKVHVIFNYKGNVNLINKDIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 197  
  
RESULT 2  
CRTC\_RAT  
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AC P18418; P10452;  
DC 01-MAR-1989 (Rel. 10, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DE 01-NOV-1997 (Rel. 35, Last annotation update)  
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (BRP60) (CALBP)  
DE (CALCIUM-BINDING PROTEIN 3) (CABP3).  
GN CALR.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain cortex;  
RX MEDLINE=90370496; PubMed=23955661;  
RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A.,  
Holmes C., Patel Y.C.;  
RT "Structural homology between the rat calreticulin gene product and  
RT the Onchocerca volvulus antigen Ral-1.";  
RL Nucleic Acids Res. 18:4933-4933(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;  
RX MEDLINE=93202172; PubMed=8453984;  
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,  
Okinaga S., Kobayashi T.;  
RT "An endoplasmic reticulum protein, calreticulin, is transported into  
RT the acrosome of rat sperm.";  
RL Exp. Cell Res. 205:101-110(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;  
RX MEDLINE=95181573; PubMed=7876339;  
RA Soennichsen B., Fueflekrug J., van Nguyen P., Diekmann W.,  
Robinson D.G., Mieskes G.;  
RT "Retention and retrieval: both mechanisms cooperate to maintain  
RT calreticulin in the endoplasmic reticulum.";  
RL J. Cell Sci. 107:2705-2717(1994).  
RN [4]  
RP SEQUENCE OF 270-358 FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;







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|||||
Db 121 GPGTKKHVIFNYKGNVINKIRCKDDETHLYTLVRENNTYEVKIDNSQVSGSLE 180
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RESULT 5
CRTC_MOUSE
ID CRTC_MOUSE STANDARD; PRT; 416 AA.
AC P14211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=90059955; PubMed=2583110;
RA Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
RT HACBP), a major calcium binding ER/SR protein.";
RL EMBO J. 8:3581-3586(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93013037; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of the sequence of an expressible cDNA clone encoding
RT ERP60/calregulin by the use of a novel nested set method.";
RL Gene 120:217-225(1992).
RN [3]
RP SEQUENCE OF 18-38.
RC TISSUE=fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X14926; CAA33053.1; -
DR EMBL; M92986; AAA37569.1; -
DR PIR; S06763; S06763.
DR PIR; JC1444; JC1444.
DR SWISS-2DPAGE; P14211; MOUSE.
DR MG; MG1:88252; Calr.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416
FT DOMAIN 18 197

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FT DOMAIN 198 308
FT DOMAIN 309 416
FT DOMAIN 417 416
FT REPEAT 191 202
FT REPEAT 203 210
FT REPEAT 211 221
FT REPEAT 222 238
FT REPEAT 239 255
FT DOMAIN 256 297
FT REPEAT 258 269
FT REPEAT 270 283
FT REPEAT 284 297
FT DOMAIN 300 407
FT DISULFID 308 317
FT SITE 413 416
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 95.8%; Score 930; DB 1; Length 416;
Best Local Similarity 94.4%; Pred. No. 2.3e-76;
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EPAYFEKEQFLDGGWTSRWIESKHKSDFGKVLSSGKFGYDEEKDKGLQTSQDAREFVAL 60
Db 18 DPAYFEKEQFLDGGWTSRWIESKHKSDFGKVLSSGKFGYDEEKDKGLQTSQDAREFVAL 77
Qy 61 SASPEPFSNKGQTLVVQFTVVKHEQIDCGGKGVKLPNLSLQDTMHGDSYENIMFGPDIC 120
Db 78 SAKTEPFSNKGQTLVVQFTVVKHEQIDCGGKGVKLPNLSLQDTMHGDSYENIMFGPDIC 137
Qy 121 GPGTKKHVIFNYKGNVINKIRCKDDETHLYTLVRENNTYEVKIDNSQVSGSLE 180
Db 138 GPGTKKHVIFNYKGNVINKIRCKDDETHLYTLVRENNTYEVKIDNSQVSGSLE 197

RESULT 6
CRTC_MOUSE
ID CRTC_MOUSE STANDARD; PRT; 406 AA.
AC P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RT calreticulin homologue.";
RL DNA Seq. 3:247-250(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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FT REPEAT      211      222      1-2.
FT REPEAT      227      238      1-3.
FT REPEAT      246      257      1-4.
FT FT DOMAIN   260      298      3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT      260      270      2-1.
FT REPEAT      274      284      2-2.
FT REPEAT      288      298      2-3.
FT FT DISULFID 105     137      BY SIMILARITY.
FT SITE        421     424      PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE    424 AA; 48350 MW; BAF27369FPB6FC37 CRC64;

Query Match          55.3%; Score 537; DB 1; Length 424;
Best Local Similarity 57.2%; Pred. No. 4.7e-41;
Matches 103; Conservative 36; Mismatches 33; Indels 8; Gaps

QY 4 VPKKEOFLDGDGWTSWIESK-HKSD--FGKFVLSGKEYGDEEKDKGLQTSDARFYAL 60
DB 21 VHPKDF-F-DND-WESRWVVDHMKDGSKGLVHTAGKWFGDENQ-KGITSEDARFYAV 77
QY 61 SASFEPSNKGOTLVQGVFKVEONIDCGGYVKLFPSNLSDTOTMHDGSEYNIMFGPDIC 120
DB 78 SAKFPSNSNGKDVLQYYVKNQEKVDCGSGTIKLPSKLDGSADFGESEYSIMFGPDVC 137
QY 121 GPCTKKVHVIFYNKGNVLINKDI-RCKDDEETHLYTLIVRPDNTYEVIDNSQVESGSL 179
DB 138 G-ASKRVHVILNYKGNHLIKKEINKEVETDLTHQTYTLVISPDNTYNYLVDNKEIQAGNL 196

RESULT 10
CRTC_EUGGR STANDARD; PRT; 401 AA.
AC Q92NV3;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Euglena gracilis.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]
RP SEQUENCE FROM N.A.
RA Navazdo L., Baldan B., Martin W., Mariani P.;
RT "Evidence for conservation of a calcium homeostat component: purification characterization and cloning of calreticulin from Euglena gracilis";
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY)
CC CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC -----
DR EMBL; Y09816; CAAT70945.1;
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; FALSE_NEG.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 401 CALRETICULIN.

```

| Matches   | 99   | Conservative  | 31          | Mismatches                                 | 43 | Indels | 6 | Gaps | 3 |
|---|--|---|-------------|--|----|--------|---|------|---|
| QY  | 4  | VYFKEQFLDGDGWT  | SRWIESKHKSD | ---FGKFVLLSSGKFGYDEEKDKGLQTSQDAFYAL        | 60 |        |   |      |   |
| Db  | 22   | VYFEERF   | --EDGWNRVK  | SDWKKDNTAGETWNTYTSCKWNGD--PNDKGIQTSDYRFVAI | 78 |        |   |      |   |
| QY  | 61   | SASFEPFSNKGQTLVQFTVKKHONIDCGGYVKLFPSNLSDQTDHGDSEYNMFGPDIC | 120         |  |    |        |   |      |   |
| Db  | 79   | SASFEPFSNKGQTLVQFTVKKHONIDCGGYVKLFPSNLSDQTDHGDSEYNMFGPDIC | 138         |  |    |        |   |      |   |
| QY  | 121  | GPCTKKVHVIFNFKGKNVLNKKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSL | 179         |  |    |        |   |      |   |
| Db  | 139  | GYSTKKVHALNNDYTHLLKKEVPCETDQLTHYTLIVRPDATYSILIDNVKQTGSL   | 197         |  |    |        |   |      |   |
| RESULT 13                                       |  |   |             |  |    |        |   |      |   |
| CRTC_PRUAR STANDARD; PRT; 421 AA.               |  |   |             |  |    |        |   |      |   |
| AC  | Q9XF98;  | 20-AUG-2001 (Rel. 40, Created)                            |             |  |    |        |   |      |   |
| DT  | 20-AUG-2001 (Rel. 40, Last sequence update)  |   |             |  |    |        |   |      |   |
| DT  | 20-AUG-2001 (Rel. 40, Last annotation update)  |   |             |  |    |        |   |      |   |
| DE  | CALRETICULIN PRECURSOR.  |   |             |  |    |        |   |      |   |
| OS  | Prunus armeniaca (Apricot).  |   |             |  |    |        |   |      |   |
| OC  | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;   |   |             |  |    |        |   |      |   |
| OC  | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  |   |             |  |    |        |   |      |   |
| OC  | eurosid I; Rosales; Rosaceae; Prunus.  |   |             |  |    |        |   |      |   |
| OX  | NCBI_TaxID=36596;  |   |             |  |    |        |   |      |   |
| RP  | SEQUENCE FROM N.A.   |   |             |  |    |        |   |      |   |
| RP  | STRAIN=CV. BERGERON; TISSUE=Mesocarp, and Endocarp;  |   |             |  |    |        |   |      |   |
| RA  | Mbeugue-A-Mbeugue D., Fils-Lycaon B.R.;  |   |             |  |    |        |   |      |   |
| RT  | "Molecular cloning and nucleotide sequence of a calreticulin from  |   |             |  |    |        |   |      |   |
| RT  | apricot (Prunus armeniaca cv. Bergeron).";   |   |             |  |    |        |   |      |   |
| RL  | Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  |   |             |  |    |        |   |      |   |
| CC  | -I- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  |   |             |  |    |        |   |      |   |
| CC  | LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  |   |             |  |    |        |   |      |   |
| CC  | -I- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).   |   |             |  |    |        |   |      |   |
| CC  | -I- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  |   |             |  |    |        |   |      |   |
| CC  | -----  |   |             |  |    |        |   |      |   |
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| CC  | the European Bioinformatics Institute. There are no restrictions on its  |   |             |  |    |        |   |      |   |
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| CC  | entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> |   |             |  |    |        |   |      |   |
| CC  | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).  |   |             |  |    |        |   |      |   |
| CC  | -----  |   |             |  |    |        |   |      |   |
| DR  | EMBL; AF134733; AAD32207.1; -  |   |             |  |    |        |   |      |   |
| DR  | InterPro; IPR001580; Calreticulin.   |   |             |  |    |        |   |      |   |
| DR  | InterPro; IPR000886; ER.target.  |   |             |  |    |        |   |      |   |
| DR  | Pfam; PF00262; calreticulin; 1.  |   |             |  |    |        |   |      |   |
| DR  | PRINTS; PR00626; CALRETICULIN.   |   |             |  |    |        |   |      |   |
| DR  | ProDom; PD001866; Calreticulin; 1.   |   |             |  |    |        |   |      |   |
| DR  | PROSITE; PS00014; ER_TARGET; 1.  |   |             |  |    |        |   |      |   |
| DR  | PROSITE; PS00803; CALRETICULIN_1; 1.   |   |             |  |    |        |   |      |   |
| DR  | PROSITE; PS00804; CALRETICULIN_2; 1.   |   |             |  |    |        |   |      |   |
| DR  | PROSITE; PS00805; CALRETICULIN_REPEAT; 2.  |   |             |  |    |        |   |      |   |
| KW  | Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  |   |             |  |    |        |   |      |   |
| FT  | SIGNAL   | 1   | 22          | POTENTIAL.                                 |    |        |   |      |   |
| FT  | CHAIN  | 23  | 421         | CALRETICULIN.                              |    |        |   |      |   |
| FT  | CARBOHYD   | 56  | 56          | N-LINKED (GLCNAC. . .) (POTENTIAL).        |    |        |   |      |   |
| FT  | CARBOHYD   | 156   | 156         | N-LINKED (GLCNAC. . .) (POTENTIAL).        |    |        |   |      |   |
| FT  | SITE   | 418   | 421         | PREVENT SECRETION FROM ER (POTENTIAL).     |    |        |   |      |   |
| SQ  | SEQUENCE   | 421 AA;   | 48416 MW;   | 4F5F94CBAA6C6690 CRC64;                    |    |        |   |      |   |
| Query Match 54.3%; Score 527; DB 1; Length 421; |  |   |             |  |    |        |   |      |   |
| Best Local Similarity 55.3%; Pred. No. 3.7e-40; |  |   |             |  |    |        |   |      |   |
| Matches   | 99   | Conservative  | 28          | Mismatches                                 | 46 |        |   |      |   |

Db 26 VFEERF--EDGWRKRVTSWKNDENLAGENWYRSGKMGD-PNDKGIQTSEDYRFAI 82  
 QY 61 SASPEFNSKGTLLVQVTVRHEQNIIDCGGVYKLFPSLSLQTDHMGSEYNIIMFGPDIC 120  
 Db 83 SAEPFNSKGTLLVQVTVRHEQNIIDCGGVYKLFPSLSLQTDHMGSEYNIIMFGPDIC 142  
 QY 121 GPGTKKVVIFNYKGNVINKDKDETHLYTLVRPDPNTYEVKIDNSQVSGSL 179  
 Db 143 GYSTKKVHAILNYNTNLIKDVPCETDQLTHVTFYIRDPATYSILIDNLEKQTGSL 201

RESULT 14  
 CRT2\_ORYSA  
 ID CRT2\_ORYSA STANDARD; PRT; 424 AA.

AC Q9SLY8;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CALRETICULIN PRECURSOR.  
 OS Oryza sativa (Rice).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Eriocarpaceae; Oryzeae; Oryza.  
 CC NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Komatsu S., Li Z.;  
 RT "Cloning the cDNA encoding a calcium-binding protein which involved in  
 the regeneration of rice cultured suspension cells.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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DR EMBL; AB021259; BAA88900.1;  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER-TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 1.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 FT SIGNAL 1 29 POTENTIAL.  
 FT CHAIN 30 424 CALRETICULIN.  
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 424 AA; 47925 MW; 3172634F1580FC14 CRC64;

Query Match 54.3%; Score 527; DB 1; Length 424;  
 Best Local Similarity 55.9%; Pred. No. 3.7e-40;  
 Matches 100; Conservative 31; Mismatches 42; Indels 6; Gaps 3;

QY 4 VYFKQFLDGGWTSRWIESKHSD---FGKVLSSGKFYGDDEKDLQTSQDARFYAL 60  
 Db 31 VYFQKFE--EDGWESWYKSEKKDKMAGENWYRSGKMGDPE-DKGIQTSEDYRFAI 87  
 QY 61 SASPEFNSKGTLLVQVTVRHEQNIIDCGGVYKLFPSLSLQTDHMGSEYNIIMFGPDIC 120  
 Db 88 SAEPFNSKGTLLVQVTVRHEQNIIDCGGVYKLFPSLSLQTDHMGSEYNIIMFGPDIC 147

QY 121 GPGTKKVVIFNYKGNVINKDKDETHLYTLVRPDPNTYEVKIDNSQVSGSL 179  
 Db 148 GYSTKKVHIFTKNDKNHLIKDVPCETDQLSHVTLIHPDATYSILIDNVEKSGSI 206

RESULT 15

CRT2\_BOVIN  
 ID CRT2\_BOVIN STANDARD; PRT; 421 AA.

AC P42918;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 CC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Brain;  
 RX MEDLINE=93385184; PubMed=8373827;  
 RA Liu N., Fine R.E., Johnson R.J.;  
 RT "Comparison of cDNAs from bovine brain coding for two isoforms of  
 calreticulin.";  
 RL Biochim. Biophys. Acta 1202:70-76(1993).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; L13462; AAC37307.1;  
 DR InterPro; IPR001580; Calreticulin.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PRODOM; PD001866; Calreticulin; 1.  
 DR PROSITE; PS00014; ER-TARGET; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 FT SIGNAL 1 34 POTENTIAL.  
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.  
 FT DOMAIN 35 201 N-DOMAIN.  
 FT DOMAIN 202 312 P-DOMAIN.  
 FT DOMAIN 313 421 C-DOMAIN.  
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.  
 FT REPEAT 195 206 1-1.  
 FT REPEAT 214 225 1-2.  
 FT REPEAT 231 242 1-3.  
 FT REPEAT 248 259 1-4.  
 FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.  
 FT REPEAT 263 273 2-1.  
 FT REPEAT 277 287 2-2.  
 FT REPEAT 291 301 2-3.  
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.  
 FT DISULFID 141 167 BY SIMILARITY.  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SITE 418 421 PREVENT SECRETION FROM ER.  
 SQ SEQUENCE 421 AA; 48612 MW; 0257E959F71528BC CRC64;

Query Match

53.8%; Score 522.5; DB 1; Length 421;

Best Local Similarity 55.6%; Pred. No. 9.4e-40;  
Matches 109; Conservative 12; Mismatches 30; Indels 45; Gaps 4;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | EPAYVFEQFLDGDGWTSRWIESKHKSD-----FGKFVLSSGKFGYGDDE           | 44  |
| Db | 35  | EERVFFSEQFLT-----LDLKYKASKLSSIREALSMKVGIIENFCFSEISFLOESI    | 86  |
| QY | 45  | KDKGLQTSQDARFYALSASFEPFSNKGQTLVQFTVKHEQNIDCGGGYVKLFPNSLDQTD | 104 |
| Db | 87  | KSHGRRT-----LVGCSPWGHE-----EQNIDCGGGYVNVFPAGLDQTD           | 125 |
| QY | 105 | MHGDSEYNIMFGPDICGPGTKKVHVIFNYKGNVLIINKDIRCKDDETHLYTLIVREDNT | 164 |
| Db | 126 | MHGDSEYNIMFGPDICGPGTKKVHVIFNYKGNVLIINKDIRCKDDETHLYTLIVREDNT | 185 |
| QY | 165 | YEVKIDNSQVESGSLE 180  |     |
| Db | 186 | YEVKIDNSQVESGSLE 201  |     |

Search completed: January 9, 2002, 15:12:14  
Job time: 656 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:58 ; Search time 78.15 Seconds  
(without alignments)  
336.904 Million cell updates/sec

Title: US-09-828-000-3

Perfect score: 971

Sequence: 1 EPAVYFREQLDGDGWSRW.....PDNTYEVKIDNSQVSGSLE 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17.\*

- 1: sp-archaea.\*
- 2: sp-bacteria.\*
- 3: sp-fungi.\*
- 4: sp-human.\*
- 5: sp-invertebrate.\*
- 6: sp-mammal.\*
- 7: sp-mhc.\*
- 8: sp-organelle.\*
- 9: sp-phage.\*
- 10: sp-plant.\*
- 11: sp-rodent.\*
- 12: sp-virus.\*
- 13: sp-vertebrate.\*
- 14: sp-unclassified.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description         |
|------------|-------|---------------|--------|-------|---------------------|
| 1          | 835   | 86.0          | 411    | 13    | Q91710 xenopus lae  |
| 2          | 804   | 82.8          | 405    | 5     | Q26268 alypsia cal  |
| 3          | 797   | 82.1          | 343    | 13    | Q91711 xenopus lae  |
| 4          | 796   | 82.0          | 419    | 13    | Q98984 rana rugosa  |
| 5          | 785   | 80.8          | 417    | 13    | Q9PU01 brachydanio  |
| 6          | 759   | 78.2          | 410    | 5     | Q16893 amblyomma a  |
| 7          | 731   | 75.3          | 421    | 5     | Q9U6S0 strongyloce  |
| 8          | 699   | 72.0          | 406    | 5     | Q9U916 drosophila   |
| 9          | 681.5 | 70.2          | 403    | 5     | Q76961 necator ame  |
| 10         | 680   | 70.0          | 387    | 5     | Q97372 dirofilaria  |
| 11         | 673   | 69.3          | 375    | 5     | Q18478 litomosoides |
| 12         | 641   | 66.0          | 380    | 11    | Q9D906 xenopus lae  |
| 13         | 539   | 55.5          | 412    | 10    | Q40040 hordeum vul  |
| 14         | 539   | 55.5          | 415    | 10    | Q40041 hordeum vul  |
| 15         | 536   | 55.2          | 421    | 10    | Q43712 zea mays (m  |
| 16         | 517   | 53.2          | 389    | 10    | Q40567 nicotiana t  |
| 17         | 514.5 | 53.0          | 427    | 10    | Q9FYV2 pinus taeda  |
| 18         | 507.5 | 52.3          | 396    | 5     | Q45034 schistosoma  |
| 19         | 477.5 | 49.2          | 350    | 5     | Q26514 schistosoma  |

|    |       |      |     |    |                    |
|----|-------|------|-----|----|--------------------|
| 20 | 464.5 | 47.8 | 240 | 10 | Q9ST29 solanum mel |
| 21 | 460   | 47.4 | 318 | 13 | Q9PTX7 lampetra re |
| 22 | 450   | 46.3 | 214 | 4  | Q9UDG2 homo sapien |
| 23 | 448.5 | 46.2 | 403 | 5  | Q9XYF8 trypanosoma |
| 24 | 446.5 | 46.0 | 401 | 5  | Q9U9N9 trypanosoma |
| 25 | 409.5 | 42.2 | 291 | 5  | Q9XIV1 leishmania  |
| 26 | 332   | 40.4 | 397 | 5  | Q94592 leishmania  |
| 27 | 373   | 38.4 | 321 | 13 | Q9U5G0 eptatretus  |
| 28 | 347   | 35.7 | 422 | 10 | O22502 brassica na |
| 29 | 329.5 | 33.9 | 321 | 10 | Q41799 zea mays (m |
| 30 | 302.5 | 31.2 | 101 | 10 | Q40751 parthenium  |
| 31 | 289.5 | 29.8 | 582 | 3  | Q9HFC6 yarrowia li |
| 32 | 270   | 27.8 | 578 | 11 | Q9D2K5 mus musculu |
| 33 | 264.5 | 27.2 | 559 | 5  | Q9NG26 tritrichomo |
| 34 | 263.5 | 27.1 | 581 | 5  | Q9BLH3 halocynthia |
| 35 | 262   | 27.0 | 622 | 13 | Q98985 rana rugosa |
| 36 | 251   | 25.8 | 70  | 10 | Q9SXW3 lithospermu |
| 37 | 248   | 25.5 | 582 | 5  | Q04702 schistosoma |
| 38 | 240   | 24.7 | 583 | 5  | Q9VXF6 drosophila  |
| 39 | 238.5 | 24.6 | 582 | 5  | O76214 schistosoma |
| 40 | 238.5 | 24.6 | 582 | 5  | Q9TVF3 schistosoma |
| 41 | 231.5 | 23.8 | 272 | 4  | Q16094 homo sapien |
| 42 | 224   | 23.1 | 543 | 5  | Q9VYP4 drosophila  |
| 43 | 224   | 23.1 | 556 | 5  | Q9I7S9 drosophila  |
| 44 | 221.5 | 22.8 | 605 | 5  | O02393 drosophila  |
| 45 | 207   | 21.3 | 545 | 5  | Q9VAL7 drosophila  |

ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| Q91710   |   |
| ID       | Q91710 PRELIMINARY; PRT; 411 AA.                                  |
| AC       | Q91710;   |
| DT       | 01-JAN-1998 (TREMBLrel. 05, Created)                              |
| DT       | 01-JAN-1998 (TREMBLrel. 05, Last sequence update)                 |
| DT       | 01-JUN-2001 (TREMBLrel. 17, Last annotation update)               |
| DE       | CALRETICULIN PRECURSOR (FRAGMENT).                                |
| OS       | Xenopus laevis (African clawed frog).                             |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC       | Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;   |
| OC       | Xenopodinae; Xenopus.   |
| OX       | NCBI_TaxID=8355;  |
| RN       | [1]   |
| RP       | SEQUENCE FROM N.A.  |
| RC       | TISSUE=BRAIN;   |
| RX       | MEDLINE=93074997; PubMed=1445218;                                 |
| RA       | Treves S., Zorzato F., Pozzan T.;                                 |
| RT       | "Identification of calreticulin isoforms in the central nervous   |
| RT       | system.";   |
| RL       | Biochem. J. 287:579-581(1992).                                    |
| DR       | EMBL; X67597; CAA47866.1; .                                       |
| DR       | InterPro; IPR000886; ER_target.                                   |
| DR       | InterPro; IPR001580; Calreticulin.                                |
| DR       | Pfam; PF00262; calreticulin; 1.                                   |
| DR       | PRINTS; PR00626; CALRETICULIN.                                    |
| DR       | ProDom; PD001866; Calreticulin; 1.                                |
| DR       | PROSITE; PS00803; CALRETICULIN_1; 1.                              |
| DR       | PROSITE; PS00804; CALRETICULIN_2; 1.                              |
| DR       | PROSITE; PS00805; CALRETICULIN_REPEAT; 2.                         |
| DR       | PROSITE; PS00014; ER_TARGET; UNKNOWN_1.                           |
| KW       | SIGNAL.   |
| FT       | NON_TER 1 1   |
| FT       | SIGNAL <1 12 POTENTIAL.   |
| FT       | CHAIN 13 411 CALRETICULIN.  |
| SQ       | SEQUENCE 411 AA; 48344 MW; 891DA66E0EBEFA CRC64;                  |

Query Match 86.0%; Score 835; DB 13; Length 411;  
Best Local Similarity 83.9%; Pred. No. 2.7e-71;  
Matches 151; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

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QY 1 EPAYVFKQFLDGDGWTNRWIESKHKSDFKFLVLSGKFGYDEKDKGLQTSQDARFYAL 60
Db 13 EPAYVFKKEEFTDGDGWTNRWESKHKTDYDKFKLSAGKFGYDSEKDKGLQTSQDARFYAM 72
QY 61 SASFPFSSKNGKQTLVVQVTVKHEQNIDCGGKFLPNSLDQTDHMGDSEYNIMFGPDIC 120
Db 73 SRSFDSFSKNGKQTLVVQVTVKHEQNIDCGGKFLPNSLDQTDHMGDSEYNIMFGPDIC 132
QY 121 GPCTKKVHVIFNKGKNNVLINKDICKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 180
Db 133 GPPTKKVHVIFQYKKNLQINKDICKDDSFTHLYTLIVRPDNTYEVKIDNSKVESGSLE 192
RESULT 2
ID Q26268 PRELIMINARY; PRT; 405 AA.
AC Q26268;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALRETICULIN.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidia;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93098937; PubMed=1463604;
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
RT calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL: S51239; A824569.1; -.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS0014; ER-TARGET; UNKNOWN_1.
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840DID69 CRC64;
Query Match 82.8%; Score 804; DB 5; Length 405;
Best Local Similarity 79.4%; Pred. No. 2,3e-68;
Matches 143; Conservative 18; Mismatches 17; Indels 2; Gaps 1;
QY 1 EPAYVFKQFLDGDGWTNRWIESKHKSDFKFLVLSGKFGYDEKDKGLQTSQDARFYAL 60
Db 16 DPTVVFKEEF--GDDWAERWVESKHKSGLGKFLTAGKFGYDAEKDKGLQTSQDARFYGL 73
QY 61 SASFPFSSKNGKQTLVVQVTVKHEQNIDCGGKFLPNSLDQTDHMGDSEYNIMFGPDIC 120
Db 74 SARFQFSNEGKTLVQTVKHEQNIDCGGKFLPNSLDQSDMHGSEYPYIMFGPDIC 133
QY 121 GPCTKKVHVIFNKGKNNVLINKDICKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 180
Db 134 GPCTKKVHVIFNKGKNNLVLKDKDDFVSHLYTLIVRPDNTYEVKIDNEKASGDL 193
RESULT 3
ID Q91711 PRELIMINARY; PRT; 343 AA.
AC Q91711;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
```

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OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=93074997; PubMed=1445218;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoforms in the central nervous
RT system.";
RL Biochem. J. 287:579-581(1992).
DR EMBL; X67598; CAA47867.1; -.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 1
FT NON_TER 343
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;
Query Match 82.1%; Score 797; DB 13; Length 343;
Best Local Similarity 85.2%; Pred. No. 8,7e-68;
Matches 144; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
QY 12 DGDGWTNRWIESKHKSDFKFLVLSGKFGYDEKDKGLQTSQDARFYALSAPFSPNKG 71
Db 1 DGDGWTNRWESKHKSDFKFLVLSGKFGYDEKDKGLQTSQDARFYAMSRRFSPNKG 60
QY 72 QTLVQVTVKHEQNIDCGGKFLPNSLDQTDHMGDSEYNIMFGPDICGCTKKVHVIF 131
Db 61 QTLVQVTVKHEQNIDCGGKFLPNSLDQTDHMGDSEYNIMFGPDICGCTKKVHVIF 120
QY 132 NYKGNKLVINKDIRCKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 180
Db 121 QYKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSKVESGSLE 169
RESULT 4
ID Q98984 PRELIMINARY; PRT; 419 AA.
AC Q98984;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALRETICULIN.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96234004; PubMed=8654561;
RA Yamamoto S., Nakamura M.;
RT "Calnexin: its molecular cloning and expression in the liver of the
RT frog, Rana rugosa.";
RL FEBS Lett. 387:27-32(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamamoto S.;
RT "Strong expression of the calreticulin gene in the liver of Rana
RT rugosa Tadpoles.";
RL J. Exp. Zool. 0:0-0(1996).
DR EMBL; D78589; BAA11425.1; -.
DR InterPro; IPR000886; ER-target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
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DE CALRETICULIN PRECURSOR.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioides;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99094497; PubMed=9879888;
RT Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;
  "Molecular Characterization of a Calcium-binding protein from the
  RT filarial parasite Dirofilaria immitis.";
  Mol. Biochem. Parasitol. 97:69-79(1998).
DR EMBL: AF052978; AD03405.1;
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; Calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Signal.
FT SIGNAL.
FT CHAIN 1 18 POTENTIAL.
FT CHAIN 19 387 CALRETICULIN.
SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AAFA5885 CRC64;

Query Match 70.0%; Score 680; DB 5; Length 387;
Best Local Similarity 68.5%; Pred. No. 1.3e-56;
Matches 122; Conservative 27; Mismatches 27; Indels 2; Gaps 2;

QY 4 VYKPEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSODARFYALSAS 63
DB 19 IYKPEFSD-DDWEKRWIKSKHKDDFGKWEISHGKFYGDVADKGLTKTQDAKFYSIGAK 77
QY 64 FEP-FSNKGQTLVQVTVKHEQNDICGGGVYKLPNSLDQTDHMGSEYNIMFGPDICGP 122
DB 78 FDGFSNKGSLVQFSVKHEQDIDCGGVYKLVMSANLEDFHGETPYHIMFGPDICGP 137
QY 123 GTKKVVHVFYKGNKLVINKDIRCKDDFTHLYTLVVRPNTVEVKIDNSQVSGSLE 180
DB 138 GTKKVVHVFYKGNKLVINKDIRCKDDVFTHLTYLTVNSDNPTEVQIDGKAESGELE 195

RESULT 12
QY 9QD906 PRELIMINARY; PRT; 380 AA.
AC 9QD906;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE 1700031L01RIK PROTEIN.
GN 1700031L01RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK006582; BAB24660.1;
DR MGD; MGI:1920566; 1700031L01RIK.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 2.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR SIGNAL.
DR CHAIN 1 18 POTENTIAL.
DR CHAIN 19 387 CALRETICULIN.
SQ SEQUENCE 380 AA; 44198 MW; B13BC4ADB1B0442 CRC64;

Query Match 66.0%; Score 641; DB 11; Length 380;
Best Local Similarity 65.0%; Pred. No. 6.4e-53;
Matches 115; Conservative 30; Mismatches 32; Indels 0; Gaps 0;

QY 4 VYKPEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSODARFYALSAS 63
DB 21 VYQEEFLDGERWRNRWVQSTNDSQFGHFRVSSGKFGYHKEKDKGLQTSNRYALSAS 80
QY 64 FEP-FSNKGQTLVQVTVKHEQNDICGGGVYKLPNSLDQTDHMGSEYNIMFGPDICGP 123
DB 81 FKPFNSNKGKTLVIQYTVKHEQDKCGGVYKLVPSLDQKMKNGKSYIIMFGPDICGFD 140

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QY 124 TKKHVHIFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVSGSL 180
||||| : : | |||| | ||||| : ||||| : ||||| :
DB 141 IKKHVHILFYKQYHKNKPIRCKVDGFTHLYTLVLRPDLSEYKVDGSGSIE 197

RESULT 13
Q40040 PRELIMINARY; PRT; 412 AA.
AC Q40040;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
GN CRH1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MOREX; TISSUE-OVARY;
RX MEDLINE-94339696; PubMed-7914763;
RA Chen F., Hayes P.M., Mulroony D., Pan A.;
RT "Identification and characterization of cDNA clones encoding plant
calreticulin in barley.";
RL Plant Cell 6:835-843(1994).
DR EMBL; L27348; AAA32948.1; -.
DR MDEL; 8546; Horvu; 1166; 8546.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR001866; Calreticulin.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Calcium-binding.
FT NON_TER 1
FT NON_TER 412
SQ SEQUENCE 412 AA; 47037 MW; 37F6C95D6AA78AB0 CRC64;

Query Match 55.5%; Score 539; DB 10; Length 412;
Best Local Similarity 56.4%; Pred. No. 3.4e-43;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY 4 VYFKEQFLDGGTWSWIESKHKSD---FGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
||:|:| ||| ||||:| | | : : ||||:| | ||||:| ||||:|
DB 20 VYFQKFAF--EDGWESRWKSEKKNMAGENNHTSGKWHGDAE-DKG|QTS|EDYRFYAI 76
|| : |||| | ||||| ||||| ||||| ||||| ||||| |||||
QY 61 SASFEPFSNKGQTLVYQVFTVKEHQNTDCGGYVKLPFPNSLDQTDHMGDSEYNIMFGPDIC 120
|| : |||| | ||||| ||||| ||||| ||||| ||||| |||||
DB 77 SAEYPEFSNKDKTLVLFQFTVKEHQKLDGCGYVKLLGGVDQKKFGGDPYGYIMFGPDIC 136
|| : |||| | ||||| ||||| ||||| ||||| ||||| |||||
QY 121 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVSGSL 179
| ||||| | ||| | | : : ||||| ||||| ||||| |||||
DB 137 GYSTKKVHTILTKNGKNHLIKKDVCPETDQLSHVYTLIRPDATYSILIDNEEKQTGSI 195

RESULT 14
Q40041 PRELIMINARY; PRT; 415 AA.
AC Q40041;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
GN CRH2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MOREX; TISSUE-OVARY;
RX MEDLINE-94339696; PubMed-7914763;
RA Chen F., Hayes P.M., Mulroony D., Pan A.;
RT "Identification and characterization of cDNA clones encoding plant
calreticulin in barley.";
RL Plant Cell 6:835-843(1994).
DR EMBL; L27349; AAA32949.1; -.
DR MDEL; 8547; Horvu; 1166; 8547.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR001866; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Calcium-binding.
FT NON_TER 1
FT NON_TER 415
SQ SEQUENCE 415 AA; 47359 MW; 2897914812FBE33E CRC64;

Query Match 55.5%; Score 539; DB 10; Length 415;
Best Local Similarity 56.4%; Pred. No. 3.4e-43;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY 4 VYFKEQFLDGGTWSWIESKHKSD---FGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
||:|:| ||| ||||:| | | : : ||||:| | ||||:| ||||:|
DB 23 VYFQKFAF--EDGWESRWKSEKKNMAGENNHTSGKWHGDAE-DKG|QTS|EDYRFYAI 79
|| : |||| | ||||| ||||| ||||| ||||| ||||| |||||
QY 61 SASFEPFSNKGQTLVYQVFTVKEHQNTDCGGYVKLPFPNSLDQTDHMGDSEYNIMFGPDIC 120
|| : |||| | ||||| ||||| ||||| ||||| ||||| |||||
DB 80 SAEYPEFSNKDKTLVLFQFTVKEHQKLDGCGYVKLLGGVDQKKFGGDPYGYIMFGPDIC 139
|| : |||| | ||||| ||||| ||||| ||||| ||||| |||||
QY 121 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVSGSL 179
| ||||| | ||| | | : : ||||| ||||| ||||| |||||
DB 140 GYSTKKVHTILTKNGKNHLIKKDVCPETDQLSHVYTLIRPDATYSILIDNEEKQTGSI 198

RESULT 15
Q43712 PRELIMINARY; PRT; 421 AA.
AC Q43712;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALCIUM-BINDING PROTEIN PRECURSOR.
GN CRT1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VAR MERIT; TISSUE=ROOT TIP;
RA Napier R.M., Trueman S., Henderson J., Boyce J.M., Hawes C.R.,
RA Fricker M.D., Venis M.A.;
RL J. Exp. Bot. 46:1603-1613(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-96309381; PubMed-8704156;
RA Dresselhaus T., Hagel C., Loerz H., Kranz E.;
RT "Isolation of a full-length cDNA encoding calreticulin from a PCR
library of in vitro zygotes of maize.";
RL Plant Mol. Biol. 31:23-34(1996).
DR EMBL; Z46772; CAA86728.1; -.
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DR EMBL; X89813; CAA61939.1; -  
DR Mendel; 11228; Zeama;1166;11228.  
DR InterPro; IPR000886; ER\_target.  
DR InterPro; IPR001580; Calreticulin.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 2.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
KW Signal; Calcium-binding.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 421 CALRETICULIN.  
SQ SEQUENCE 421 AA; 48012 MW; 5AAE02B77ED3126D CRC64;  
  
Query Match 55.2%; Score 536; DB 10; Length 421;  
Best Local Similarity 56.4%; Pred. No. 6.7e-43;  
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;  
  
QY 4 VFKEQFLDGDGWTGRWIESHKSD--FGKVLSSGKFGYGDDEKDKGLQTSQDARFYAL 60  
Db 27 VFFQEKF--EDGWESRWKSEWKKDENWAGWNHTSGKWNGDAE--DKGIQTSEDYRFYAI 83  
  
QY 61 SASFEPFNKGQTLVVQFTVKHEQNIIDCGGYVVKLFPSLSLQDTMDHGDSEYNIMFGPDIC 120  
Db 84 SAEYEPFSNKDKTLVLQFSVKHEQKLDCCGGYVVKLLGGDVQDKFEGGDTYSIMFGPDIC 143  
  
QY 121 GPGTKVHVIFNYKKNVLIINKDIRCKDDEFTHLVTLIVRPDNTYEVKIDNSQVSSGL 179  
Db 144 GYTRKKVHTILT KDGNHLIRKDPVCPETDQLTHVYTLIIRPDATYSILIDNEEKQTGSI 202

Search completed: January 9, 2002, 15:03:27  
Job time: 269 sec

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